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(54) Title: **HIGH THROUGHPUT MULTIPLEX DNA SEQUENCE AMPLIFICATIONS**

Criteria Used in Designing Primers That Are Experimentally Acceptable	
Tm Range of the primers (°C)	75-103
Length of the primers (bp)	24-33
Number of consecutive matching bases between the 3' ends of any two primer molecules	<4
Number of consecutive matching bases with one mismatch between the 3'-ends of any two primer molecules	<7
Number of consecutive matching bases between the 3'-end of one primer molecule and anywhere in another primer molecule	<9
Number of consecutive matching bases with one mismatch between the 3'-end of one primer molecule and anywhere in another primer molecule	<11
Maximal number of matching bases between two primer molecules	<75%
Number of consecutive matching bases between the 3'-end a primer molecule and anywhere in a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	12
Number of consecutive matching bases with one mismatch between the 3'-end of a primer molecule and anywhere in a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	15
Maximal number of matching bases between a primer molecule and a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	<80%

(57) Abstract: The present invention provides methods of designing PCR primers that allow the efficient and simultaneous amplification of a large number of different desired DNA fragments in a single multiplex PCR and minimize the formation of nonspecific extensions of undesired DNA fragments. The present invention allows a multiplex PCR to use at least 50 pairs of primers and produce at least 50 DNA fragments of interest. The present invention significantly broadens the application of multiplex PCR in the identification of multiple genes related to multifactorial diseases, the genome-scale detection of genetic alterations, the studies in large-scale pharmacogenetic reactions, the genotyping genetic polymorphism in a large population, the gene expression profiling in various samples, and high throughput genotyping technologies.

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High Throughput Multiplex DNA Sequence AmplificationsReference to Government Grant

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rights in this invention.

Field of the Invention

This invention pertains to the field of high throughput multiplex DNA sequence
amplification. Specifically, the invention pertains to methods of designing primers that allow
10 the simultaneous amplification of a multiplicity of DNA fragments in a single polymerase
chain reaction and minimize the formation of nonspecific extension of undesired DNA
fragments.

Background

The polymerase chain reaction (PCR) is a primer-directed *in vitro* reaction for the
15 enzymatic amplification of a specific DNA fragment. Saiki, Enzymatic Amplification of β -
Actin Genomic Sequences and Restriction Site Analysis for Diagnosis of Sickle Cell Anemia,
Science 230: 1350-54 (1985). The PCR process is involved in the repetitive cycles of
denaturation, primer annealing and extension by a thermostable DNA polymerase of two
oligonucleotide primers that flank the DNA region of interest in a template DNA sample. At
20 the beginning the PCR process, the duplex DNA target is denatured into two separated
strands of DNA through a first heating step. In a subsequent annealing step, each
oligonucleotide primer anneals or hybridizes to the complementary sequence of one separated
strand of the target DNA. In a third extension step, nascent DNA is synthesized by extending

each primer from its 3' hydroxyl end of towards the 5' end of the annealed target DNA strand by a thermostable DNA polymerase. The heating or denaturation step, the primer annealing step and the enzymatic extension step together constitute a single PCR cycle. If the newly synthesized DNA strand extends to or beyond the region complementary to the other primer, it serves as a primer annealing site and a template for extension in a subsequent PCR cycle. As a result, the repetitive PCR cycles give rise to the exponential accumulation of a specific DNA fragment whose termini are defined by the 5' ends of the two primers. Theoretically, at the n th cycle of the PCR process, a single DNA molecule can produce 2^n progeny DNA fragments of interest.

The distinctive nature of the PCR process in producing a substantive quantity of DNA fragments of interest from an initial tiny amount of DNA sample has gained broad applications in the field of biomedical research and clinical diagnosis. For example, PCR has been widely used in the diagnosis of inherited disorder and the individualization of evidence samples in the forensics area. Erlich *et al*, Recent Advances in the Polymerase Chain Reaction, *Science* 252: 1643-51 (1991); Newton & Graham, PCR (Oxford, 1994). In particular, PCR has played a critical role in genotyping a vast number of genetic polymorphisms and individual variations which underlie the onset of many diseases. Shi, Enabling Large-Scale Pharmacogenetic Studies by High-throughput Mutation Detection and Genotyping Technologies, *Clin. Chem.* 47: 164-172 (2001).

Widespread applications notwithstanding, the use of PCR is quite often limited by cost, time, and the availability of adequate test samples. To illustrate, the human genome project has placed over 6000 DNA markers in human genetic mapping. To analysis these 6000 markers in 1000 specimens, a total of 6,000,000 PCR reactions are needed if only one

marker sequence is amplified in each reaction. As a well equipped laboratory may process 300 reactions and post-PCR assay a day, it will take a total of 20,000 working days or 80 years to complete the analysis, provided that the amount of each specimen suffices 6000 reactions.

5 In overcoming these limitations, a variant PCR termed multiplex PCR has been developed. Chamberlian *et al*, Deletion Screening of the Duchenne Muscular Dystrophy Locus via Multiplex DNA Amplification, *Nucleic Acids Res.* 16: 11141-56 (1988). Unlike the standard or uniplex PCR where only one pair of primers is used to amplify a single DNA fragment of interest, the multiplex PCR includes more than one pair of primers and thus
10 results in more than one DNA fragment. Since its inception, the multiplex PCR has been applied in many areas of DNA testing, including gene deletion analysis, Chamberlain, *supra*, mutation and polymorphism analysis, Rithidech *et al*, Combining Multiplex and Touch Down PCR to Screen Murine Microsatellite Polymorphism, *Bio-Techniques* 23: 36-45 (1997), quantitative analysis, Zimmermann *et al*, Quantitative Multiple Competitive PCR of HIV-
15 DNA in a Single Reaction Tube, *BioTechniques* 21: 480-484 (1996), RNA detection, Zou, Identification of New Influenza B virus Variants by Multiplex Reverse Transcription-PCR and the Heteroduplex Mobility Assay, *J. Clin. Microbiol.* 36: 1544-1548 (1998), and identification of microorganisms, Elnifro *et al*, Multiplex PCR: Optimization and Application in Diagnostic Virology, *Clin. Microbiol. Rev.* 13: 559-570 (2000).

20 Conceptually, the multiplex PCR has the potential to produce considerable savings in cost, time and sample volume. In aforementioned project of analyzing 6000 DNA markers in 1000 specimens, if n pairs of primers are used in a multiplex PCR reaction, it will only cost one- n th of 20,000 working days to complete the project as well as one- n th of the cost and

sample volume required in the uniplex PCR reactions. Despite the attractive potential, the application of the multiplex PCR poses many challenges. For example, even under carefully optimized reaction conditions, only 26 DNA fragments could be amplified simultaneously in a single multiplex PCR. Edwards & Gibbs, Multiplex PCR: Advantages, Developments and Applications, *PCR Meth. Appl.* 3: S65-75 (1994); Lin *et al*, Multiplex Genotype Determination at a Large Number of Gene Loci, *Proc. Natl. Acad. Sci. USA* 93: 2582-2587 (1996).

Researchers are facing two tiers of challenge in optimizing the multiplex PCR. The first tier of challenge is the efficacy of PCR. In general, this issue is ubiquitous in all PCR reactions, whether in multiplex PCR or uniplex PCR. The efficacy of PCR is measured by its specificity, efficiency and fidelity. A highly specific PCR will generate one and only one amplified DNA fragment of intended sequence from each pair of primers. More efficient amplification will generate more products with fewer PCR cycles. A high-fidelity PCR product has the minimal amount of DNA polymerase-induced errors. Studies have shown the efficacy of PCR is affected by factors including the primer annealing temperature, the activity and concentration of the thermostable DNA polymerase, the PCR buffer components such as dNTPs and MgCl₂, and the first cycle set-up. Roux, Optimization and Troubleshooting in PCR, *PCR methods Appl.* 4: S185-S194 (1995); Roberston & Walsh-Weller, An Introduction to PCR Primer Design and Optimization of Amplification Reactions, *Methods Mol. Biol.* 98: 121-154 (1998). Special attention has also been paid to the primer parameters, such as homology of primers with their target DNA sequence, primer length, GC content, ratio of primers to the template DNA. Researchers are cautioned that the efficacy of PCR is often a delicate balance among specificity, efficiency and fidelity. Cha & Thilly, Specificity,

Efficiency, and fidelity of PCR, *PCR Methods. Appl.* 3: S18-S19 (1993). Adjusting the conditions for specificity may compromise the efficiency or fidelity and *visé versa*.

The second tier of challenge in multiplex PCR is the presence of multiple pairs of primers that are unique to multiplex PCR. It is reported that the presence of more than one primer pair increases the chance of obtaining spurious amplification products, primarily because of the formation of nonspecific DNA extensions, e.g., primer dimers. Markoulatos *et al*, Multiplex Polymerase Chain Reaction: A Practical Approach, *J. Clin. Lab. Anal.* 16: 47-51 (2002). The nonspecific extensions occur when 1) a first primer non-specifically interacts with a second primer because the first primer shares a certain degree of complementarity in its 3' sequence with the 3' sequence of the second primer; and 2) when a primer non-specifically interacts with a DNA sequence of a template DNA which is not the target DNA sequence. Elnifro, *supra*. The nonspecific extensions undermine not only the specificity of PCR but the efficiency as well. The nonspecific products compete with desired target DNA, consume the limited supplies of enzymes, primers and nucleotides, and produce impaired rates of annealing and extension. Markoulatos, *supra*. Not surprisingly, the non-specific extension limits the number of desired DNA fragments in a single multiplex PCR and poses a major limitation to the application and efficacy of multiplex PCR. Lin *et al*, Multiplex Genotype Determination at a Large Number of Gene Loci, *Proc. Natl. Acad. Sci. USA* 93: 2582-2587 (1996).

So far little progress has been made in combating the nonspecific extension problem. Researchers have developed a method to lower the chance of forming the nonspecific extension by adding a universal tail sequence to the 5' end of the sequence-specific primers.

Lin *et al, supra*; Brownie et al, The Elimination of Primer-Dimer Accumulation in PCR, *Nucleic Acids Res.* 25: 3235-3241 (1997). The tailed primers are added in a multiplex PCR reaction at very low concentrations and allowed to participate the early cycles of reaction. In subsequent cycles, the primers complementary to the universal tail sequence are added into the reaction at high concentrations and proceeded to continue PCR cycles. This method has reportedly produced 26 DNA fragments and minimized the accumulation of non-specific extensions. Lin *et al, supra*. However, the addition of a tail sequence does not thoroughly tackle the problem of non-specific interaction among primers or between a primer and a target DNA.

Thus, there is a need in the art to design primers that allow the simultaneous amplification of a multiplicity of DNA fragments in a single polymerase chain reaction. There is a need in the art to design primers that minimize or substantially reduce the formation of nonspecific extension of undesired DNA fragments. There is a need in the art to design primers that significantly enhance the efficacy of multiplex polymerase chain reactions.

Brief Description of the Drawings

Fig. 1 is an illustration of five forms of primer-primer interactions.

Fig. 2 is an illustration of three forms of interactions between primers and nonspecific target templates.

Fig. 3 is an illustration of a genotyping microarray determining the genotypes of a DNA sample at the 627 loci.

Fig. 4 is an illustration of a set of criteria in designing primers that are experimentally acceptable.

Summary of the Invention

One aspect of the present invention relates to methods of designing PCR primers that allow the efficient and simultaneous amplification of a large number of different desired DNA fragments in a single multiplex PCR and minimize the formation of nonspecific extensions of undesired DNA fragments.

In one embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a first primer and a second primer or the first primer comprises the steps of aligning the first primer and the second primer and selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer.
- 5) the maximal match between the first primer and the second primer does not exceed 75%.

In another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and a non primer-specific region of the a

template DNA comprises the steps of aligning the primer and the template DNA and selecting a primer wherein:

- 1) the primer at its 3' end does not contain 13 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and 2) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.

In another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions in a multiplex PCR comprises the steps of selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer;
- 5) the first primer at its 3' end does not contain 15 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary;

6) the primer at its 3' end does not contain 18 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

7) the maximal match between the first primer and the second primer used in the multiplex amplification does not exceed 75%.

Another aspect of the present invention relates to computer products or computer programs which, once executed by a computer process, perform methods as disclosed in the present invention.

The methods according to the present invention increase the number of desired DNA fragments, enhance the efficacy of the multiplex PCR and achieve a significant reduction in cost, time and sample volume. A single multiplex PCR using primers designed by the present invention can contain at least 50 pairs of primers and produce at least 50 desired DNA fragments.

The methods according to the present invention significantly broaden the application of multiplex PCR in the identification of multiple genes related to multifactorial diseases, the genome-scale detection of genetic alterations, the studies in large-scale pharmacogenetic reactions, the genotyping genetic polymorphism in a large population, the gene expression profiling in various samples, and high throughput genotyping technologies which include oligonucleotide ligation assay, pyrosequencing, single-base extension with fluorescence detection, homogeneous solution hybridization, molecular beacon genotyping, DNA chip-based microarray, and mass spectrometry technology.

Detailed Description of the Invention

The primary aspect of the present invention provides methods of designing PCR primers that allow the efficient and simultaneous amplification of a large number of different desired DNA fragments in a single multiplex PCR and minimize the formation of nonspecific extensions of undesired DNA fragments.

The nonspecific extension of unwanted DNA fragments is a major factor in preventing effective applications of multiplex PCR. The nonspecific extension is caused by nonspecific interactions between different molecules of either the same primer, or different primers, or a primer and a non-primer specific region of DNA templates. Specifically, the nonspecific interactions are caused by 1) a stretch of perfectly matched sequence at the 3' ends of two primers, 2) a stretch of perfectly matched sequence with only one mismatch at the 3' ends of two primers, 3) a stretch of the 3' end sequence of a primer perfectly matching to the internal sequence of the same primer, another primer, or a non-primer specific region of a DNA template, 4) a stretch of the 3' end sequence of a primer perfectly matching with only one mismatch to the internal sequence of itself, another primer, or a non-primer specific region of a DNA template, or 5) a stretch of a sequence in a primer matching to itself, another primer, or a non-primer specific region of a DNA template. Fig. 1. The nonspecific extensions of undesired DNA fragments compete and consume the same reagent components in the PCR reaction and thus impair the production and extension of desired DNA fragments. The problem of nonspecific extensions is aggravated when multiple pairs of primers of high concentrations are present in a single multiplex PCR.

One embodiment of the present invention circumvents the nonspecific extension by setting forth a list of criteria in designing PCR primers useful for multiplex PCR. According

to one embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and all the rest of primers including the primer comprises the steps of selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are
5 perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are
10 perfectly matching to a sequence anywhere of the first primer or the second primer; and
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer.

The same method repeatedly applies to the selection of a subsequent primer until all
15 the selected primers meet the above criteria.

According to another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and a non primer-specific region of the a template DNA comprises the steps of selecting a primer wherein:

- 1) the primer at its 3' end does not contain 13 or more bases that are perfectly
20 matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

2) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.

According to another embodiment of the invention, the method of designing primers
5 to minimize the nonspecific extensions in a multiplex PCR comprises the steps of selecting a first primer wherein:

5) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;

6) the first primer at its 3' end does not contain seven or more bases that are
10 perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;

7) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;

8) the first primer at its 3' end does not contain eleven or more bases that are
15 perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer,

9) the first primer at its 3' end does not contain 13 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

20 10) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.

In practicing the present invention, each primer to be used in a multiplex PCR is selected through the methods described herein. The selection of primers for a large number of DNA templates can be conducted manually or through a computer system. In a preferred embodiment, the methods according to the present invention are conducted through the use of
5 a computer system.

A computer system according to the present invention refers to a computer or a computer readable medium designed and configured to perform some or all of the methods as described herein. A computer used herein may be any of a variety of types of general-purpose computers such as a personal computer, network server, workstation, or other computer
10 platform now or later developed. As commonly known in the art, a computer typically contains some or all the following components, for example, a processor, an operating system, a computer memory, an input device, and an output device. A computer may further contain other components such as a cache memory, a data backup unit, and many other devices. It will be understood by those skilled in the relevant art that there are many possible
15 configurations of the components of a computer.

A processor used herein may include one or more microprocessor(s), field programmable logic arrays(s), or one or more application specific integrated circuit(s). Illustrative processors include, but are not limited to, Intel Corp.'s Pentium series processors, Sun Microsystems' SPARC processors, Motorola Corp.'s PowerPC processors, MIPS
20 Technologies Inc.'s MIPS processors, and Xilinx Inc.'s Vertex series of field programmable logic arrays, and other processors that are or will become available.

A operating system used herein comprises machine code that, once executed by a processor, coordinates and executes functions of other components in a computer and

facilitates a processor to execute the functions of various computer programs that may be written in a variety of programming languages. In addition to managing data flow among other components in a computer, an operating system also provides scheduling, input-output control, file and data management, memory management, and communication control and
5 related services, all in accordance with known techniques. Exemplary operating systems include, for example, a Windows operating system from the Microsoft Corporation, a Unix or Linux-type operating system available from many vendors, any other known or future operating systems, and some combination thereof.

A computer memory used herein may be any of a variety of known or future memory
10 storage devices. Examples include any commonly available random access memory (RAM), magnetic medium such as a resident hard disk or tape, an optical medium such as a read and write compact disc, or other memory storage devices. A memory storage device may be any of a variety of known or future devices, including a compact disk drive, a tape drive, a removable hard disk drive, or a diskette drive. Such types of memory storage device typically
15 read from, and/or write to, a computer program storage medium such as, respectively, a compact disk, magnetic tape, removable hard disk, or floppy diskette. Any of these computer program storage media, or others now in use or that may later be developed, may be considered a computer program product. As will be appreciated, these computer program products typically store a computer software program and/or data. Computer software
20 programs, also called computer control logic, typically are stored in system memory and/or the program storage device used in conjunction with memory storage device.

In one embodiment, a computer program product as described herein comprising a computer memory having a computer software program stored therein, wherein the computer

software program when executed by a processor or in a computer performs methods according to the present invention.

An input device used herein may include any of a variety of known devices for accepting and processing information from a user, whether a human or a machine, whether local or remote. Such input devices include, for example, modem cards, network interface cards, sound cards, keyboards, or other types of controllers for any of a variety of known input function. An output device may include controllers for any of a variety of known devices for presenting information to a user, whether a human or a machine, whether local or remote. Such output devices include, for example, modem cards, network interface cards, sound cards, display devices (for example, monitors or printers), or other types of controllers for any of a variety of known output function. If a display device provides visual information, this information typically may be logically and/or physically organized as an array of picture elements, sometimes referred to as pixels.

As will be evident to those skilled in the relevant art, a computer software program of the present invention can be executed by being loaded into a system memory and/or a memory storage device through one of the above input devices. On the other hand, all or portions of the software program may also reside in a read-only memory or similar type of memory storage device, such devices not requiring that the software program first be loaded through input devices. It will be understood by those skilled in the relevant art that the software program or portions of it may be loaded by a processor in a known manner into a system memory or a cache memory or both, as advantageous for execution.

As will be appreciated by those skilled in the art, a computer program product of the present invention, or a computer software program of the present invention, may be stored on

and/or executed in a PCR instrument. For example, a computer software of the present invention can be installed in, for example, the Smart Cycler System, the Idaho Rapid Cycler, the Carbett Roter-Gene System, the GeneAmp 5700 Sequence Detection System, the ABI Prism7000, 7700 & 7900 Sequence Detection Systems, the iCycler System, the MX-4000
5 Multiplex Quantitative PCR System, the DNA Engine Opticon System, the Perkin-Elmer 9600 cycler, and MJ Research's DNA Engine Opticon System.

However, it is not necessary that the computer program product or the computer software program be stored on and/or executed in a PCR instrument. Rather, the computer product or software may be stored in a separate computer or a computer server which may or
10 may not connect to the PCR instrument through a data cable, a wireless connection, or a network system. As commonly known in the art, network systems comprise hardware and software to electronically communicate among computers or devices. Examples of network systems may include arrangement over any media including Internet, Ethernet 10/1000, IEEE 802.11x, IEEE 1394, xDSL, Bluetooth, 3G, or any other ANSI approved standard.

15 In a preferred embodiment, a computer program termed MULTIPLEX is developed to select primers according to the methods as described in the present invention. See Table I for the flowchart of MULTIPLEX program.

Even with the assistance of MULTIPLEX, it is time consuming to analyze exhaustively all possible sequences frames and select the best possible frames for PCR
20 primers. To expedite the computer-assisted selection process, a strategy termed "random fitting" is developed. Under the random fitting strategy, a set of criteria for the length of the matching sequences is set forth for primer selection. See Table I.. For example, when the number of 3' end matching bases is less than 4, the experimental effect of this

complementarity is neglected. Therefore, the criterion for the length of 3' end complementarity was set to be less than four. With the predefined criteria, the MULTIPLEX computer program first randomly picks up a pair of primers for each target sequence. All possible interacting pairs in this combination are examined. Record is made on qualified and
5 unqualified primers in the combination. The program then randomly picks up a new pair of primers for each target sequence that collectively form a second combination. If the number of qualified primers in the second combination is less than that in the first combination, no record is made. The MULTIPLEX program, however, begins to examine a third combination. If the number of qualified primers in the third combination is greater than that
10 in the first combination, the first primer combination is replaced by the third one in record. The program keeps processing until a combination with all qualified primers is found. Under the random fitting strategy, the MULTIPLEX program can select qualified primers for 100 sequences within two hours, 500 within two days and 1,000 within two weeks. The "qualified primers" are those primers fully conforming with the selection criteria set forth in the method
15 of the present invention.

To further improve the MULTIPLEX program, another primer selection method called linear primer selection is also used as an alternative. See Table I. With this strategy, instead of selecting the frames randomly, each frame of a pair is selected from one end of the defined range of a sequence. The selected frame pair is then examined. If these frames are
20 qualified as primer sequences, the selection of primers for the corresponding sequence is completed. Otherwise, the selection will be continued by sliding the frames by one base toward the other ends of the sequences. The newly selected frames are then examined. If these frames are qualified as primer sequences, the selection of primers for the corresponding

sequence is then completed. Otherwise, the selection will be continued by sliding the frames by one base toward the other ends of the sequences... If the frames are slid to the other ends but not qualified frames are found, the lengths of the frames will be increased by 1 base. The same process described above will be repeated. The sliding and length changing process repeats until a pair of qualified frames is found. If no qualified frames can be found after exhausting all possible frames for a sequence, the sequence will be labeled as unusable, and will be excluded from the multiplex set. This method is called linear primer selection.

When the number of sequences is large, the random primer selection method may be used for selecting primers of only a fraction of sequences. The random selection process is stopped at a point defined by the user. The program can then switch to linear primer selection method. We have shown that appropriate combination of these two methods can increase the selection speed by several tens to >100 fold compared with using the random method only.

It needs to be pointed out that the MULTIPLEX method can be used not only for primer selection of SNPs, but also for primer selection of any other DNA and RNA sequences if a position is defined so that it can be used to separate a sequence into two parts for selecting the two primers, respectively.

Following the selecting and synthesizing of qualified primers, DNA templates are contacted with multiple primers for the amplification of desired DNA fragments under conditions suitable for multiplex PCR developed in the inventor's laboratory. These conditions are: 2.0 mM MgCl₂, 50 mM KCl, 100 mM Tris-HCl, pH 8.3, 100 μM deoxynucleotide triphosphates (dNTPs), and 10 units/50 μl "HotStart" *Taq* DNA polymerase (Qiagen, Valencia CA). The PCR mix is first preheated for 15 min at 94°C to activate the DNA polymerase followed by 40 PCR cycles. Each cycle consists of a denaturation step at

94°C for 40 sec, and then an annealing step at 55°C for 2 min followed by a ramping step from 55°C to 70°C within 5 min. After the PCR cycles, the samples are incubated at 72°C for 3 min.

A DNA template to be used in practicing the present invention includes without
5 limitation eukaryotic, prokaryotic and viral DNA. The DNA may be obtained from any cell source or body fluid. Non-limiting examples of cell sources available in clinical practice include blood cells, buccal cells, cervicovaginal cells, epithelial cells from urine, fetal cells, or any cells present in tissue obtained by biopsy. Body fluids include blood, urine, cerebrospinal fluid, semen and tissue exudates at the site of infection or inflammation. DNA
10 is extracted from the cell source or body fluid using any of the numerous methods that is standard in the art. It will be understood that the particular method used to extract DNA will depend on the nature of the source. The preferred amount of DNA to be extracted for use in the present invention is at least 5 pg which is corresponding to about 1 human cell equivalent of a genome size of 4×10^9 base pairs.

15 A primer designed in accordance to the method in the present invention is from 17 to 50 nucleotides in length, preferably 20 to 35 nucleotides in length. The concentration of a primer in the multiplex PCR reaction can range from 0.1nM to about 4μM per reaction, preferably from 1nM to 0.1 4μM per reaction.

Multiplex PCR reactions are carried out using manual or automatic thermal cycling.
20 Any commercially available thermal cycler may be used, such as, e.g., a Perkin-Elmer 9600 cycler.

The resultant multiple amplified DNA fragments of interest are analyzed using any of several methods that are well-known in the art. For example, agarose or polyacrylamide gel

electrophoresis is used to rapidly resolve and identify each of the amplified sequences. When a gel is used, different amplified sequences are preferably of distinct sizes and thus can be resolved in a single gel. The reaction mixture can further be treated with one or more restriction endonucleases prior to electrophoresis. Alternative methods of product analysis include without limitation dot-blot hybridization with allele-specific oligonucleotides, single-strand conformational polymorphism analysis, high-throughput genotyping platforms including oligonucleotide ligation assay, pyrosequencing, single-base extension with fluorescence detection, homogeneous solution hybridization, molecular beacon genotyping, DNA chip-based microarray, and mass spectrometry technology.

The multiple primers designed in accordance to the method in the present invention minimize the nonspecific interaction between primers or between a primer and nonspecific target sequence of a template DNA. Accordingly, the use of these primers in a multiplex PCR minimizes the formation of non-specific extension of undesired DNA fragments and maximizes the specific interaction and amplification of desired DNA fragments.

Furthermore, the method in the present invention increases the number of desired DNA fragments, enhances the efficacy of the multiplex PCR and achieves a significant reduction in cost, time and sample volume. Finally, the multiple primers designed in accordance with the methods of the present invention may be used in real time PCR or multiplex real time PCR.

A single multiplex PCR using primers designed by the present invention can contain at least 50 pairs of primers and produce at least 50 desired DNA fragments. It is preferred that the single multiplex PCR contain at least 100 pairs of primers and produce at least 100 desired DNA fragments.

The present invention significantly broadens the application of multiplex PCR in the art which has been limited by the nonspecific extensions of unwanted DNA fragment and the number of desired DNA fragments it could produce. Given a large number of multiple desired DNA fragments that a multiplex PCR now can produce using primers designed under the present invention, the multiplex PCR can now be fully used in applications including but not limited to the identification of multiple genes related to multifactorial diseases, the genome-scale detection of genetic alterations in cancers, the studies in large-scale pharmacogenetic reactions, the genotyping genetic polymorphism in a large population, and the gene expression profiling in various samples.

The following examples are intended to further illustrate the present invention without limiting the invention thereof.

EXAMPLE 1. Selection of 627 pairs of primers.

648 single nucleotide polymorphism (SNP) markers were initially selected from the SNP Database maintained by the National Center for Biotechnology Information. To facilitate the genotyping after PCR, all these SNPs were transition polymorphisms that were A to G or C to T changes at their polymorphic sites. All SNP sequences were analyzed by the computer program MULTIPLEX to determine whether these SNP sequences are unique in the genome. The repetitive sequences were discarded. PCR primers were selected by using the computer program MULTIPLEX described above with the following values: T_m range = 75-104°C, primer length range = 24-33 bases, 3' perfect matches <4, 3' match with 1 mismatch <7, 3' end matching internal sequences of other molecules <9; 3' end matches internal sequences of other molecules with 1 mismatch <11; maximal match between different molecules, 75%). The quality of each pair of primers was examined individually by using them to amplify their

target sequences. Only the primer pairs with high specificity and yield, as judged by gel electrophoresis, were used for multiplex amplification. At the end, a panel of 627 SNPs was selected from the initial 648 SNPs as shown in Table II and Table III. Table II is an illustration of a list of 627 single nucleotide polymorphism (SNP) markers selected from 648 SNP markers. Table 3 is an illustration of a list of 627 pairs of primers and probes that were designed according to the method disclosed in the embodiment of the invention, used in a single multiplex PCR reaction, and used for genotype determination by analyzing the multiplex PCR products by microarray.

EXAMPLE 2. Using 622 pairs of selected primers in a single multiplex PCR.

For the multiplex PCR, lysate for 500 cells from a tissue cultured cell line, MG2314, was prepared. The reason for using cells instead of purified DNA is that they could be precisely quantified and equal number of nearly equal number of copies of the target sequences could be used as the starting material. PCR mix contained 1 X PCR buffer (100 mM Tris-HCl pH 8.3, 150 mM KCl, 1.5 mM MgCl₂, and Gelatin 100 µg/ml), primers (10 nM each) for all SNPs, the four dNTPs (100 µM each), Taq DNA polymerase (5 units) with a final volume of 30 µl. Sample was preheated for 15 min at 95°C. Each PCR cycle consisted of a denaturation step at 95°C for 40 sec; annealing at 55°C for 3 min; and a step for both annealing and extension with temperature ramping from 55°C to 70°C within 5 min. A 3 min incubation at 95 °C as added after the PCR cycle to minimize the incompletely extended PCR products. PCR was completed after 40 cycles.

EXAMPLE 3. Analysis of multiple DNA fragments after the multiplex PCR

To resolve the allelic products in the multiplex PCR product for genotype determination, single base extension and microarray methods were used. Two

oligonucleotides with completely complementary sequences for each SNP were synthesized for this purpose. One of these was called E probe that was using in the single base extension assay. The other was called A probe that was spotted onto a coated glass slide. E probes had sequences with their 3'-ends next to their polymorphic sites. In the single base extension
5 assay, dideoxynucleotides labeled with either the chromophore Cy 3 or Cy 5 were used. The allelic base at the polymorphic site determined which fluorescently labeled nucleotide could be incorporated into an E probe.

The corresponding A probes were spotted onto a glass slide with a microarrayer manufactured by Cartesian. The fluorescently labeled E probes were hybridized with the A
10 probes on the microarray. The signal intensity for the alleles of each SNP was determined by using the computer software for image analysis from Biodiscovery. See, Fig. 3.

To validate the results from microarray analysis, the genotypes of the cell line used in the study were determined for all 622 SNPs by restriction enzyme digestion method described by Li & Hood, Multiplex Genotype Determination at A DNA Sequence Polymorphism
15 Cluster in The Human Immunoglobulin Heavy-Chain Region, *Genomics* 26: 199-206 (1995). A few SNPs that could not be analyzed by this method were analyzed by direct sequence analysis.

Because all SNP were transition polymorphisms, all E probes could be analyzed by either A and G or T and C. In either case, consistent results from 85% (for labeling with A
20 and G) to 90% (for labeling with T and C) SNPs were obtained by both microarray and the restriction digestion methods. A probes for A and G labeling were used for 85% of SNPs, and others were replaced by those for T and C labeling. Fig. 5.

Papers and patents listed in the disclosure are expressly incorporated by reference in their entirety. It is to be understood that the description, specific examples, and figures, while indicating preferred embodiments, are given by way of illustration and exemplification and are not intended to limit the scope of the present invention. Various changes and
5 modifications within the present invention will become apparent to the skilled artisan from the disclosure contained herein. Therefore, the spirit and scope of the appended claims should not be limited to the description of the preferred versions contained herein.

Flow Chart - General

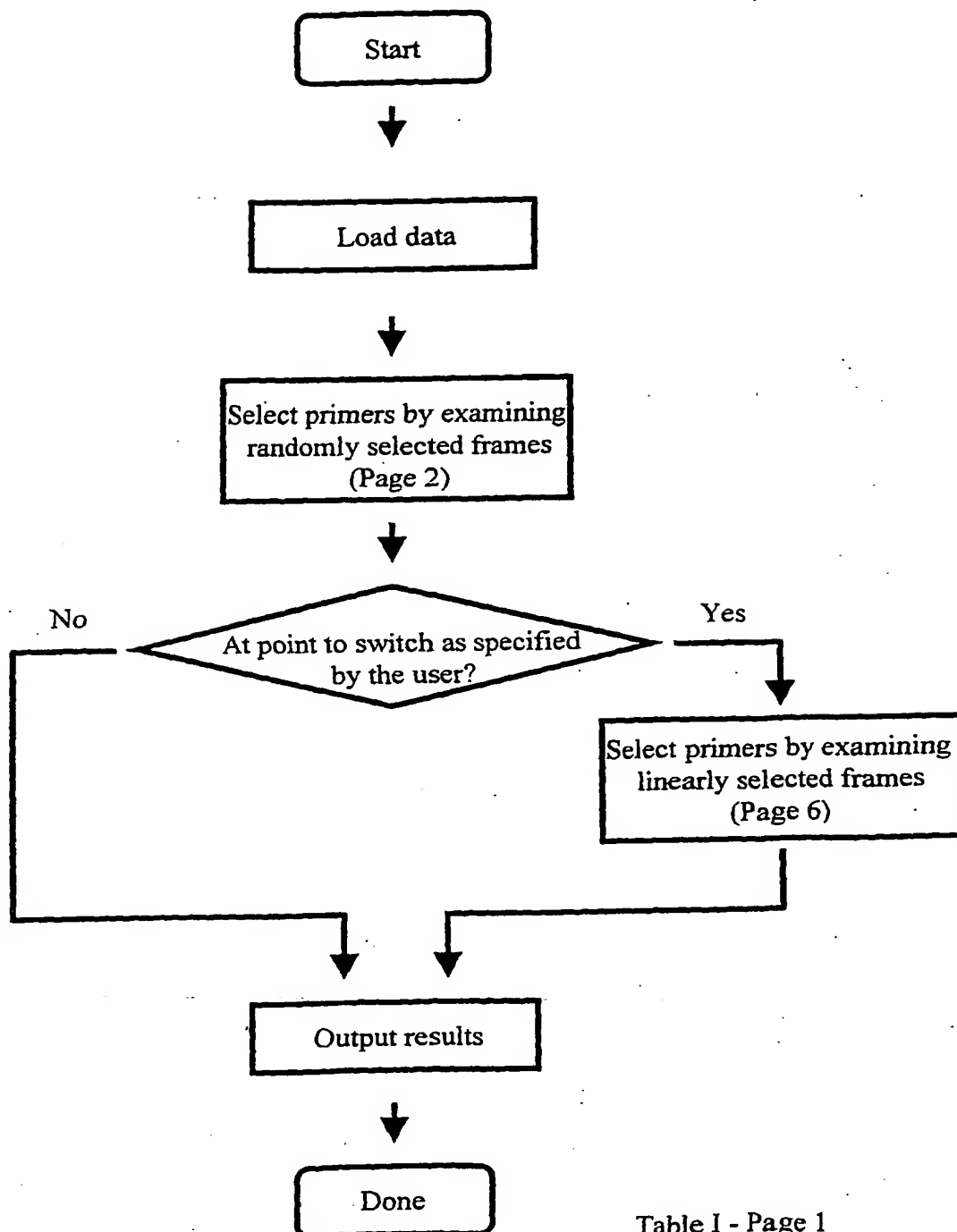


Table I - Page 1

Page 2 – Select Primers by Examining Randomly Selected Frames

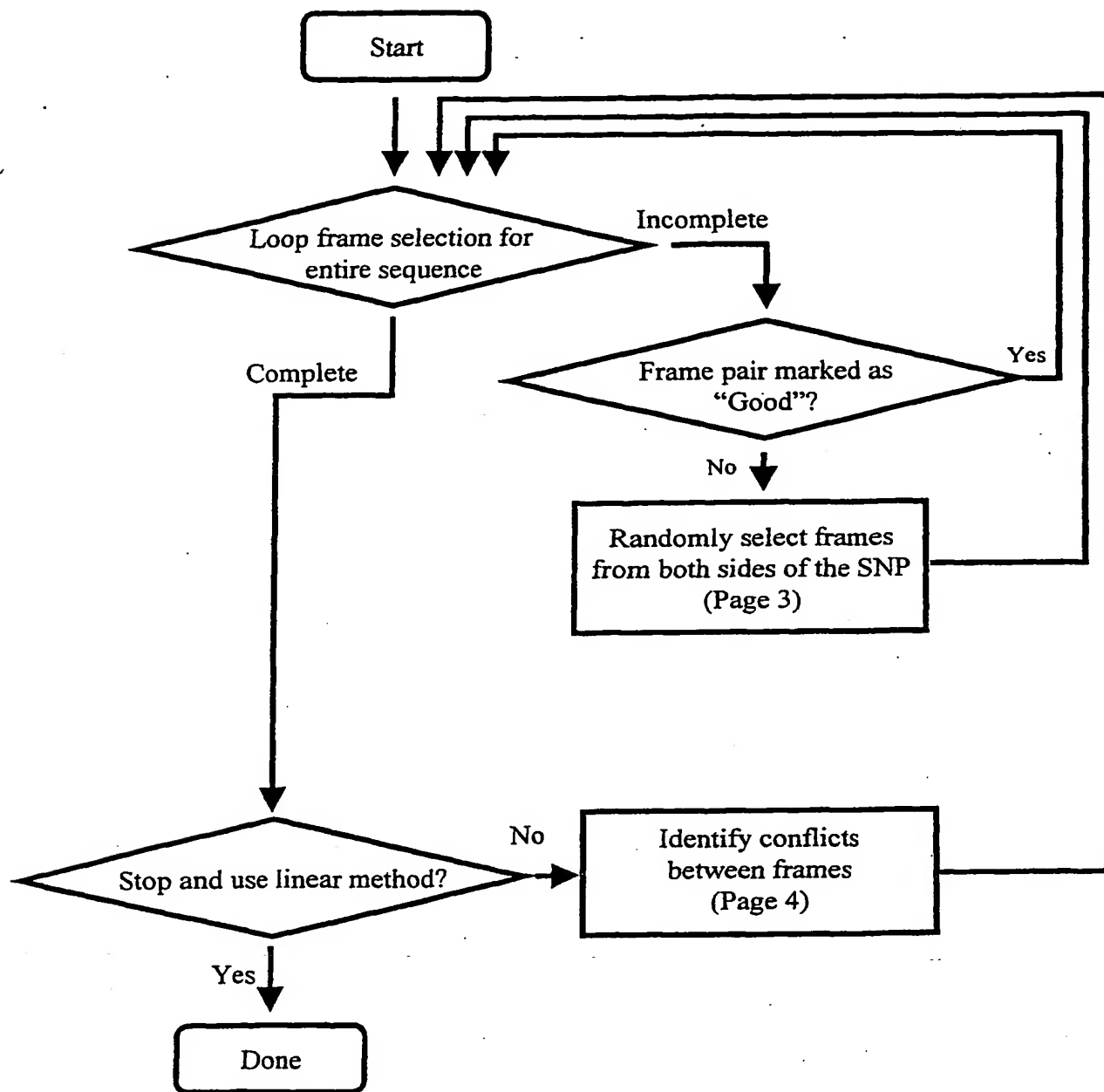


Table I - Page 2

Page 3 - Randomly Select Frames from Both Sides of Each SNP

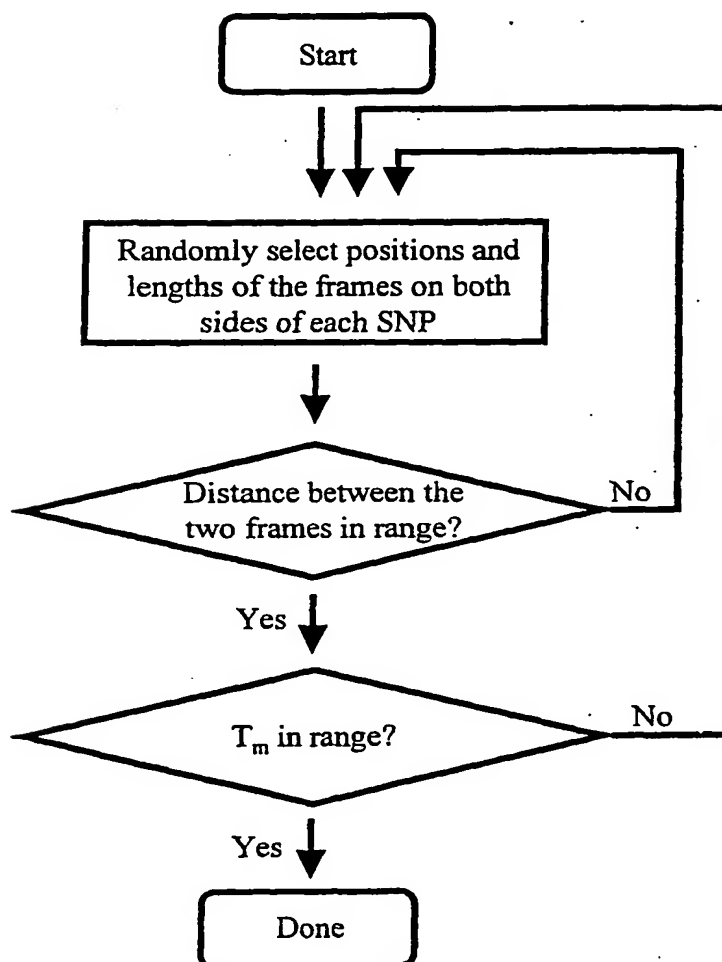


Table I - Page 3

Page 4 - Identify Conflicts between Frames

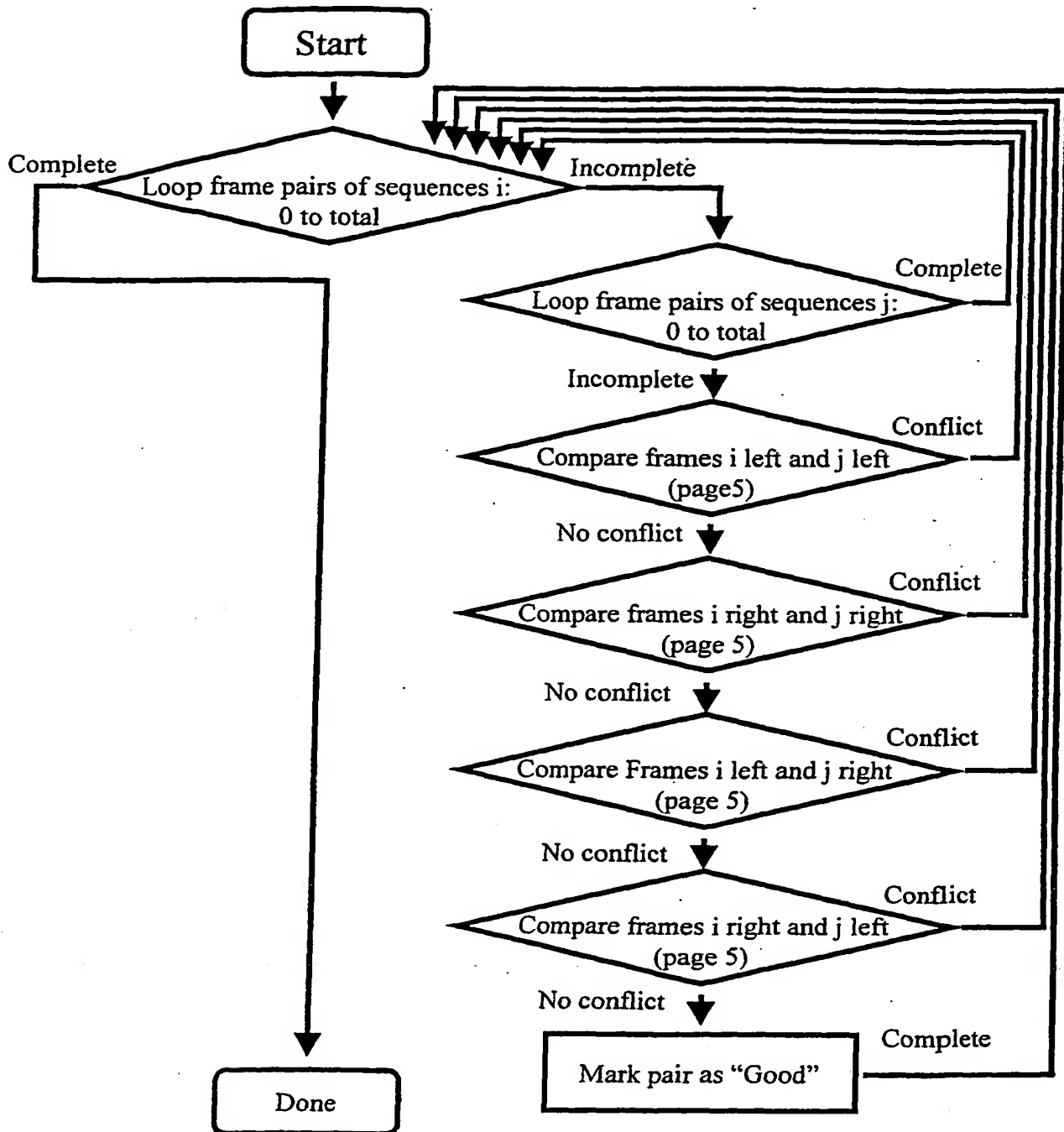


Table I - Page 4

Page 5 – Compare Selected Frames

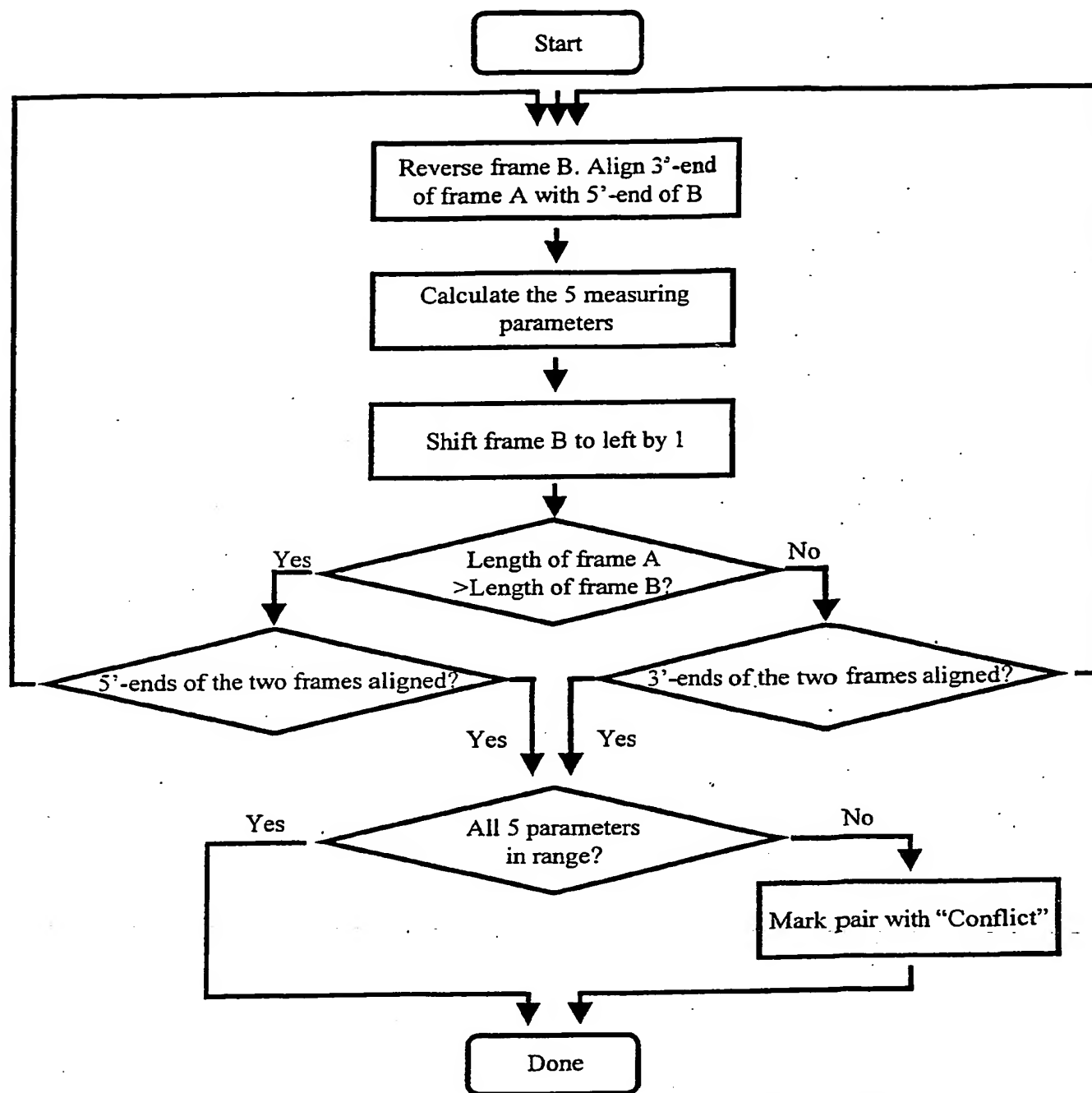


Table I - Page 5

Page 6 - Select Primers by Examining Linearly Selected Frames

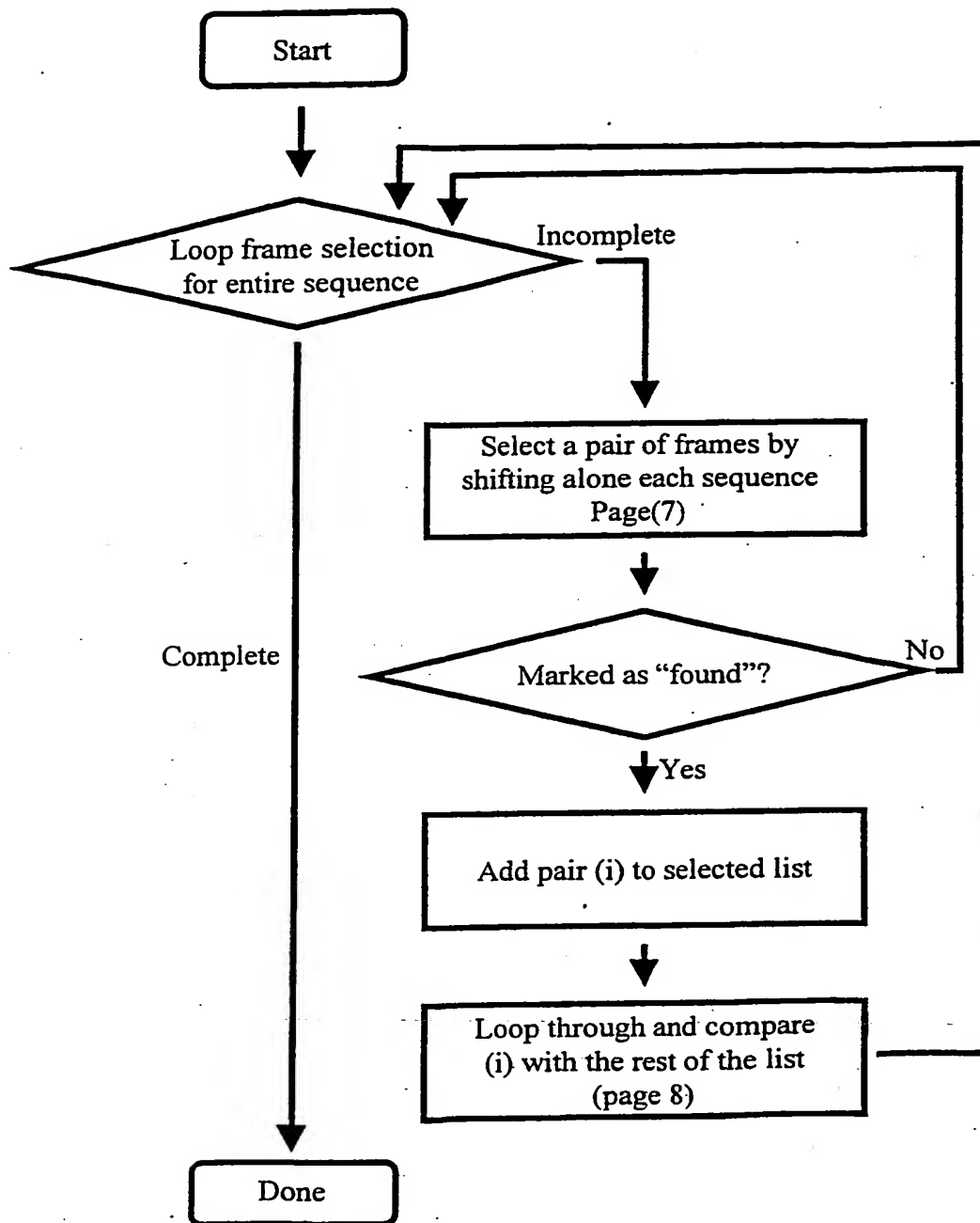


Table I - Page 6

Page 7 – Select a pair of frames by shifting along each sequence

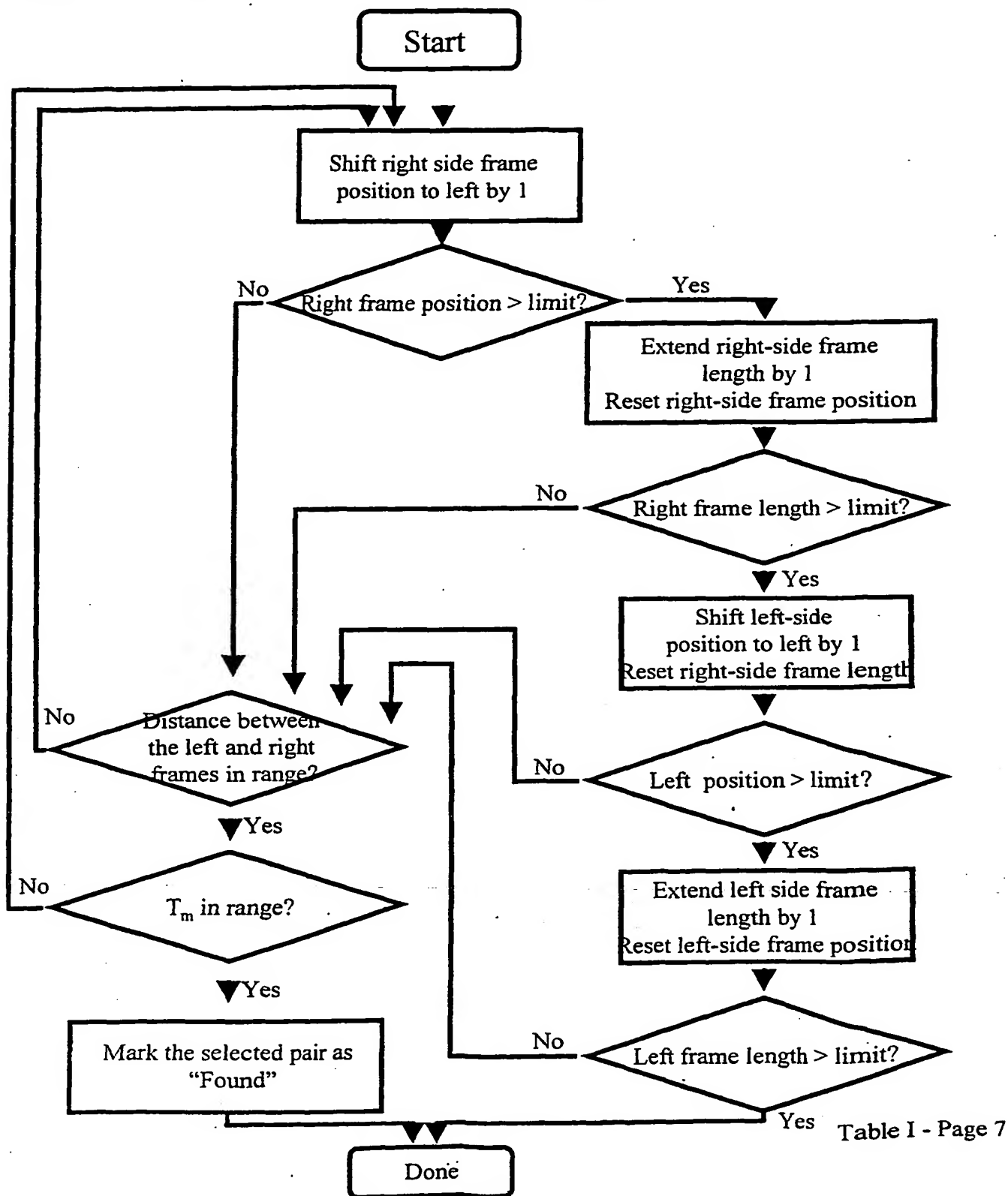


Table I - Page 7

Page 8 - Loop through and Compare Frames i with the Rest of the List

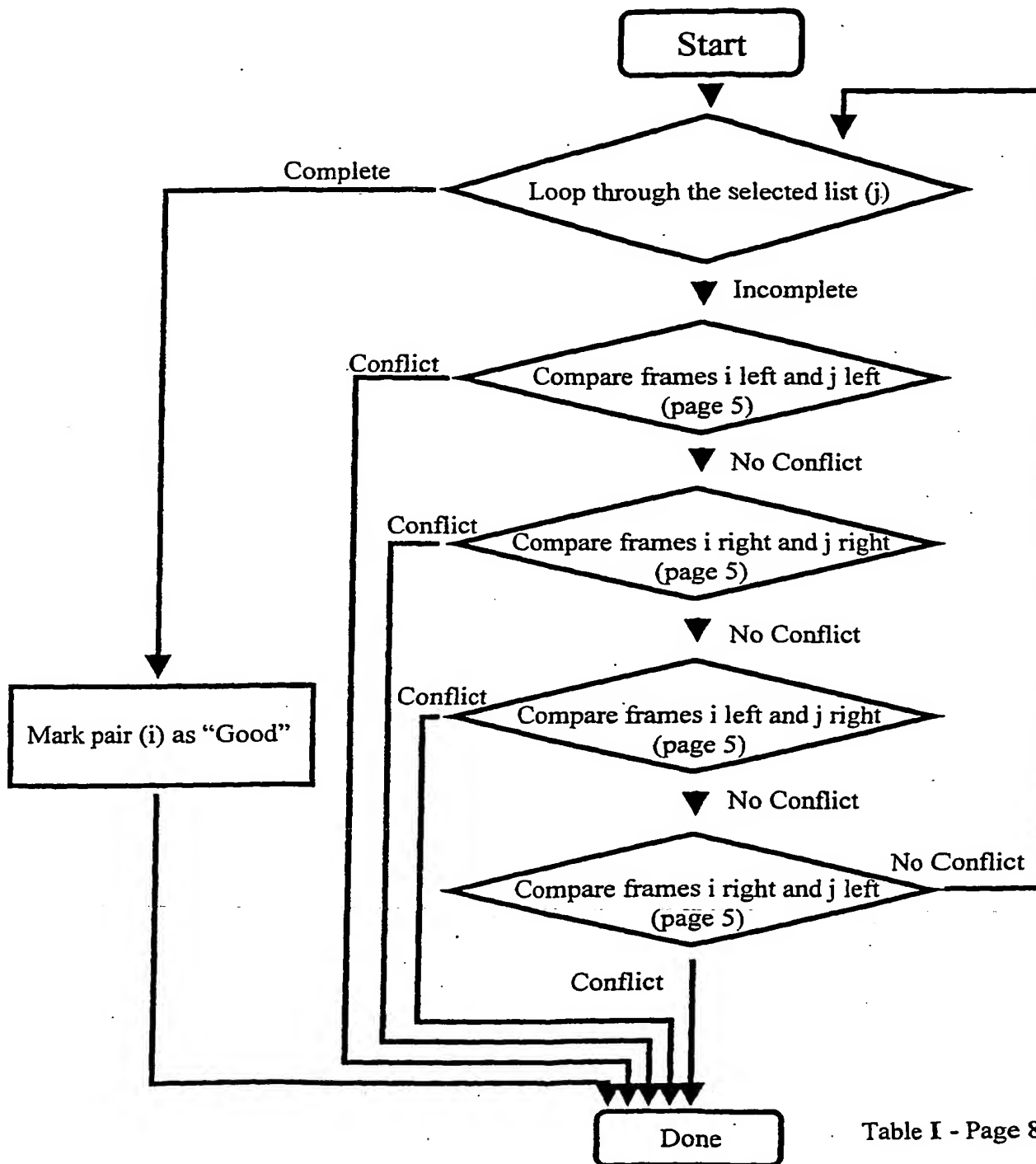


Table 2 Oligonucleotides Used as PCR Primers and as Probes for Genotyping

SNP	Left Primer			Right Primer			Labial Probe			Primer on Slide		
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')
01T002L	01T002L	CACGTGTGAGGCGCTTG0GTCC	01T002R	GCTCTACGCTGGGACACTGGGGGGG	01T002E	GCTCCGCACTGCTTCCCGCGAGTC	01T002A	GATCTGGGGGAAAGGCAATGGGAGC	01T002A	GATCTGGGGGAAAGGCAATGGGAGC	01T002A	GATCTGGGGGAAAGGCAATGGGAGC
01T003L	01T003L	CTATAGCCCTCTGAAATGCTC	01T003R	TTCTGCGCTTCCCGACAGACAC	01T003E	GCTGAAAGCAATATGGGTGTACAGAC	01T003A	GCTGTGACACCAATATGCTTTCAGC	01T003A	GCTGTGACACCAATATGCTTTCAGC	01T003A	GCTGTGACACCAATATGCTTTCAGC
01T006L	01T006L	AAAGAAAGGAGGATTTTGGGGAT	01T006R	CACAATGCTGACGACCGAGAGACTC	01T006E	CTTATTAACAGCTAGAAATATGATGTC	01T006A	GCAATCTAAATTTCTAGCTGTAATGAAG	01T006A	GCAATCTAAATTTCTAGCTGTAATGAAG	01T006A	GCAATCTAAATTTCTAGCTGTAATGAAG
01T008L	01T008L	ACTAAGAGGAGCACTAACACTC	01T008R	AAGCACTCTCTCTACGATCC	01T008E	CATCTGTGGGGGTCTGTGACCC	01T008A	GGTGTGACAGGCGCCCAAGCAGTC	01T008A	GGTGTGACAGGCGCCCAAGCAGTC	01T008A	GGTGTGACAGGCGCCCAAGCAGTC
01T009L	01T009L	GTACGGTGTCTACAGGACCAACCA	01T009R	GGGAGCACTCTGTAGTGGGGGCG	01T009E	GCTGCTGGGGGTCTGTGGCTTAA	01T009A	TTACGCGCCAGGCGCCCAAGCAGC	01T009A	TTACGCGCCAGGCGCCCAAGCAGC	01T009A	TTACGCGCCAGGCGCCCAAGCAGC
01T012L	01T012L	CAACTTGAAGTATGATGATATGGGA	01T012R	TAGCAATCCCAAGCTCTGTGA	01T012E	GAATTAATTTCTGCACTTATCTAATCTC	01T012A	GAGATTAATTAAGTGTGAGGAATTAATCTC	01T012A	GAGATTAATTAAGTGTGAGGAATTAATCTC	01T012A	GAGATTAATTAAGTGTGAGGAATTAATCTC
01T013L	01T013L	GAATTTCTATCTCACACCGGTGA	01T013R	AGGCTGCTCTGCTTCCACAC	01T013E	GCTTTATACAGAGGGGTATATAAAGGT	01T013A	ACCTTTTATACCCCTGCTGTATAAGC	01T013A	ACCTTTTATACCCCTGCTGTATAAGC	01T013A	ACCTTTTATACCCCTGCTGTATAAGC
01T014L	01T014L	ACAGCTGTATCAAGAAGTCC	01T014R	TCTTCTCTGATGCTCTAATG	01T014E	GCCACAGATAGTGTGTGAGGATTTTGA	01T014A	TTCAAAAGTGTGTGAACTTACTCTGTGCCC	01T014A	TTCAAAAGTGTGTGAACTTACTCTGTGCCC	01T014A	TTCAAAAGTGTGTGAACTTACTCTGTGCCC
01T019L	01T019L	ACTGCCACCTCTGCEAGAAGCTA	01T019R	GTCTTCTCTGCGAGCTCCC	01T019E	GCCCATTAATTTCTTCCACTTTGCT	01T019A	GTCAAAAGTGTGTGAACTTACTCTGTGCCC	01T019A	GTCAAAAGTGTGTGAACTTACTCTGTGCCC	01T019A	GTCAAAAGTGTGTGAACTTACTCTGTGCCC
01T020L	01T020L	ACACCTCTGTGCGATATAGTAG	01T020R	GAATGGATGAGGACACTCAAAAT	01T020E	GCTTAAGAGGCGCCACACATCTCTG	01T020A	CAGGAATGTCTGGGTCTCTTTAAGCC	01T020A	CAGGAATGTCTGGGTCTCTTTAAGCC	01T020A	CAGGAATGTCTGGGTCTCTTTAAGCC
01T023L	01T023L	AGATTTTCTTGACGCTCTCTTA	01T023R	AAAGGATGATTAACAAGGTGAC	01T023E	TTGGCCAGCTGGCAATCAAGAGGAC	01T023A	GTCTCTTCTATGCTACTGCGCAAA	01T023A	GTCTCTTCTATGCTACTGCGCAAA	01T023A	GTCTCTTCTATGCTACTGCGCAAA
01T025L	01T025L	AAGGATAAAGCTCACTGACTTGGGA	01T025R	GTACAATGCCGTGTGCAAGC	01T025E	GTGATCAATCAATTAACATAGGGCAT	01T025A	AGCCAGGCTATGATAGGCAATGCTC	01T025A	AGCCAGGCTATGATAGGCAATGCTC	01T025A	AGCCAGGCTATGATAGGCAATGCTC
01T028L	01T028L	CCACGGGAAGCTGTGGAATAG	01T028R	GAAGGACATCGGGTCTGTCTCCC	01T028E	AGGCAAGGCGAGGGGAGGGT	01T028A	AACTCTCTCTGCTCTTCTGCTCT	01T028A	AACTCTCTCTGCTCTTCTGCTCT	01T028A	AACTCTCTCTGCTCTTCTGCTCT
01T029L	01T029L	ATTATGAGCTTATGTAATTTAG	01T029R	GAGGCAAGGCTTTTAATTC	01T029E	GGTCTAAGAGCTGACTCTGCCACTTA	01T029A	TAAGTGTGCAATGATGATGCTTGAACCC	01T029A	TAAGTGTGCAATGATGATGCTTGAACCC	01T029A	TAAGTGTGCAATGATGATGCTTGAACCC
01T032L	01T032L	CAAAAGACTCAAGTCTTAAAAA	01T032R	TATACACCAAGGACAAAAA	01T032E	TTTATAGGAGCTTGTGCCAATACCT	01T032A	AGGTATGCGCAAGGATCTCTTAAC	01T032A	AGGTATGCGCAAGGATCTCTTAAC	01T032A	AGGTATGCGCAAGGATCTCTTAAC
01T035L	01T035L	GTCTCATGAGCCGACCGGGG	01T035R	AGGCTGTGAGCAGCGGCAC	01T035E	GCTGAGCAGCGCCCGGTGGCCG	01T035A	CGGCGACCGGGCGTCTTAAC	01T035A	CGGCGACCGGGCGTCTTAAC	01T035A	CGGCGACCGGGCGTCTTAAC
01T037L	01T037L	GCATCAGTAACTGACAACTCTAA	01T037R	CCTGAGCCCTAGTGTGCTG	01T037E	CTGGCCCTGTACTAGTTCTTGAAGG	01T037A	CTTCTCAAGAACTAGTACAGGGCCAG	01T037A	CTTCTCAAGAACTAGTACAGGGCCAG	01T037A	CTTCTCAAGAACTAGTACAGGGCCAG
01T038L	01T038L	TCTTAGCAGGGGGAACAGC	01T038R	TCAAGGCTCTTCTAACGGACTC	01T038E	CACCAAGGCTATGATGATGATGATG	01T038A	GGGTGATTTGTATGAGGCAATGCTG	01T038A	GGGTGATTTGTATGAGGCAATGCTG	01T038A	GGGTGATTTGTATGAGGCAATGCTG
01T039L	01T039L	CTCTAGTAAACCGCATACACCT	01T039R	GECCTCTCAGAGGCTTCAAT	01T039E	GAATCAATCAATTAACATAGGGCAT	01T039A	AGCCAGGCTATGATAGGCAATGCTC	01T039A	AGCCAGGCTATGATAGGCAATGCTC	01T039A	AGCCAGGCTATGATAGGCAATGCTC
01T041L	01T041L	TCTCCAGTGAAGTCTGGGGGCTGG	01T041R	GTGAACTGAGGCTGGAGAGTGG	01T041E	GGCCAGCTGTGCTTCTACGGCTGGCT	01T041A	AGCCAGGCTATGATAGGCAATGCTC	01T041A	AGCCAGGCTATGATAGGCAATGCTC	01T041A	AGCCAGGCTATGATAGGCAATGCTC
01T042L	01T042L	CTCATCTGAGCTAGGCGCTCCGC	01T042R	AGGAAAGATGATGCGAGGAACA	01T042E	CGCCAGCTGCTCTTCCCAACAGGC	01T042A	GCTCTGTGGGAAAGGACACTGGG	01T042A	GCTCTGTGGGAAAGGACACTGGG	01T042A	GCTCTGTGGGAAAGGACACTGGG
01T043L	01T043L	ATTCTGAACTTTCTACGCAC	01T043R	ATTCTAGGCCCTAGGCCAGACTTA	01T043E	CACCAGAGGCGCTTGTGAACACAGA	01T043A	GCTCTGTGGGAAAGGACACTGGG	01T043A	GCTCTGTGGGAAAGGACACTGGG	01T043A	GCTCTGTGGGAAAGGACACTGGG
01T046L	01T046L	TCTGAACACCCCGGTTTATAG	01T046R	GGTCTCATGTTGATCCCTAT	01T046E	GAAGAGATATATGCCCATGTTATCAAAA	01T046A	TTTGTATACATGGGGATATATCTCTTC	01T046A	TTTGTATACATGGGGATATATCTCTTC	01T046A	TTTGTATACATGGGGATATATCTCTTC
01T047L	01T047L	CAGAGGCTTGGCGTTTGCTCTTIA	01T047R	AAGGCACTGCAGACTTTTIAGITTA	01T047E	TCTATAGGCATGTGTAGTATCTCACTG	01T047A	CATGTGATATACACCACTGCTATATAGA	01T047A	CATGTGATATACACCACTGCTATATAGA	01T047A	CATGTGATATACACCACTGCTATATAGA
01T048L	01T048L	CCACACCTTAGAAGCGTGTA	01T048R	AAAAACTCCAGTCTCTTGCG	01T048E	TAGCCCATGTAGACGTAGAGGATGA	01T048A	TCATCCTCACTGCTCTCATGCTCTCA	01T048A	TCATCCTCACTGCTCTCATGCTCTCA	01T048A	TCATCCTCACTGCTCTCATGCTCTCA
01T051L	01T051L	CTACCTCGCTCTGGGCGCTTG	01T051R	CTCATCTTTTCTTCTCATAGCAT	01T051E	TGTGATTTGGGCGGGGTGTGGG	01T051A	CCACACCTACCCGCCCAACAATCA	01T051A	CCACACCTACCCGCCCAACAATCA	01T051A	CCACACCTACCCGCCCAACAATCA
01T054L	01T054L	TGAGATGGCGGCACTCCGTG	01T054R	GCTCTGTTTTACTTCCAACT	01T054E	GGAGTGTGTGACCTGTACAGTGCCA	01T054A	CCCTCTGTGAGGCGGCATCTCTGC	01T054A	CCCTCTGTGAGGCGGCATCTCTGC	01T054A	CCCTCTGTGAGGCGGCATCTCTGC
01T055L	01T055L	CTGTGGGCGGTGTACAGGAACCT	01T055R	TTAGTGGAAATCTCAAGCT	01T055E	CGAGATGTGGCTCTTCCACAGAGG	01T055A	TGCACTGTGTACAGCTACACACATG	01T055A	TGCACTGTGTACAGCTACACACATG	01T055A	TGCACTGTGTACAGCTACACACATG
01T056L	01T056L	CACAATGGACAAATAATCCAAAC	01T056R	GGTAGTGGGGAATGTGTGGTGAAT	01T056E	CCATGTGTGTGACTGTACAGTGCCA	01T056A	TGTGAGATGTGTGTGTGTGTGTGAAT	01T056A	TGTGAGATGTGTGTGTGTGTGTGAAT	01T056A	TGTGAGATGTGTGTGTGTGTGTGAAT
01T057L	01T057L	CCATTAAGCAATGACACAGCTTG	01T057R	AAAAACCAACAAAATCTATGGCTA	01T057E	CTCTCTCTGAAAAAGAGATAGTCTTCA	01T057A	TGTAAAGATCTATCTCTTTTTCACGGAAG	01T057A	TGTAAAGATCTATCTCTTTTTCACGGAAG	01T057A	TGTAAAGATCTATCTCTTTTTCACGGAAG
01T058L	01T058L	GTGTCGGCGTGGCATATGATG	01T058R	CACCACTAAAAGGATAACTCTAA	01T058E	CTCGTCCGAAGCATGAAGGATTA	01T058A	TAATCCTCTATGCTTGGGACAGGATTC	01T058A	TAATCCTCTATGCTTGGGACAGGATTC	01T058A	TAATCCTCTATGCTTGGGACAGGATTC
01T060L	01T060L	GGACTGCTACTACACAATGGAGGTA	01T060R	TGCTTGGATGAGTGTGTTCTGGT	01T060E	GGAGATTAATGCTGGAAATAAGAAATCC	01T060A	GGCAGAGGACTAGGCTGAAGGATTC	01T060A	GGCAGAGGACTAGGCTGAAGGATTC	01T060A	GGCAGAGGACTAGGCTGAAGGATTC
01T061L	01T061L	CACGGCTGTGCAAGGGGTTGGGTA	01T061R	GGATAGAACTCTCCCTCGTGCTC	01T061E	GAATCTTCAAGCTAGTCTCTGCGC	01T061A	TGTTGAGATGTGTGTGTGTGTGAAT	01T061A	TGTTGAGATGTGTGTGTGTGTGAAT	01T061A	TGTTGAGATGTGTGTGTGTGTGAAT
01T062L	01T062L	AAATGTGTACATGGTCTTGTGAO	01T062R	ACTAAACCTCTCTGGGATGGCA	01T062E	ATTTCACTACACAACACTCAACA	01T062A	TGTTGAGATGTGTGTGTGTGTGAAT	01T062A	TGTTGAGATGTGTGTGTGTGTGAAT	01T062A	TGTTGAGATGTGTGTGTGTGTGAAT
01T063L	01T063L	ATTCATACATAAATATGCAACT	01T063R	AGCTTTTGAATTTCCCACTGCT	01T063E	GCAATACCTCTTAACATCATATGTAAT	01T063A	TGTTGAGATGTGTGTGTGTGTGAAT	01T063A	TGTTGAGATGTGTGTGTGTGTGAAT	01T063A	TGTTGAGATGTGTGTGTGTGTGAAT
01T064L	01T064L	GTGTGCTCTACAAAGAAAGCG	01T064R	TTATGCACTATAACCTTCTGTGAT	01T064E	AAATTAATCTTTTCAAAAAATATGACGTAA	01T064A	TGTTGAGATGTGTGTGTGTGTGAAT	01T064A	TGTTGAGATGTGTGTGTGTGTGAAT	01T064A	TGTTGAGATGTGTGTGTGTGTGAAT
01T065L	01T065L	GCCACTCTGATGAGTATCTTIA	01T065R	GACAGATTTTCTGTGCTCTTAA	01T065E	CTAGCAAGCATGAGGCGGTATCTG	01T065A	TGTTGAGATGTGTGTGTGTGTGAAT	01T065A	TGTTGAGATGTGTGTGTGTGTGAAT	01T065A	TGTTGAGATGTGTGTGTGTGTGAAT
01T066L	01T066L	TTGAAGTGTGTGTGTGTGTATGCCA	01T066R	CTCACACTCAAGGGGAA	01T066E	AGTACGTAGGCCCTTGTACCCCTT	01T066A	TGTTGAGATGTGTGTGTGTGTGAAT	01T066A	TGTTGAGATGTGTGTGTGTGTGAAT	01T066A	TGTTGAGATGTGTGTGTGTGTGAAT
01T067L	01T067L	ADAGGATATCTGTATAACTGATAAA	01T067R	CGAGTGTCTTGGCCACACCCCTTGG	01T067E	GAAGATAATACACCAACCACTCTTCTTA	01T067A	TGTTGAGATGTGTGTGTGTGTGAAT	01T067A	TGTTGAGATGTGTGTGTGTGTGAAT	01T067A	TGTTGAGATGTGTGTGTGTGTGAAT
01T068L	01T068L	TACAATGCTTTTCTTCAACAT	01T068R	TGTGTAGTCACTCATTTATGCTTA	01T068E	TCCCTTAAAAATGCTAGGCAACTCTTCTTA	01T068A	TGTTGAGATGTGTGTGTGTGTGAAT	01T068A	TGTTGAGATGTGTGTGTGTGTGAAT	01T068A	TGTTGAGATGTGTGTGTGTGTGAAT
01T069L	01T069L	TATCCCTCTGCCATCTGGGGA	01T069R	AAATTTCTAGTACATGTGTCAGTGA	01T069E	CCCTTAAAGCAAGTGTGTCACCACTT	01T069A	TGTTGAGATGTGTGTGTGTGTGAAT	01T069A	TGTTGAGATGTGTGTGTGTGTGAAT	01T069A	TGTTGAGATGTGTGTGTGTGTGAAT
01T070L	01T070L	TTGCTCTCAGTGTAGTATG	01T070R	CTTTCGCCCTACATTTTCTTCC	01T070E	CAAGATGTACATTTCTCTTAAAGCA	01T070A	TGTTGAGATGTGTGTGTGTGTGAAT	01T070A	TGTTGAGATGTGTGTGTGTGTGAAT	01T070A	TGTTGAGATGTGTGTGTGTGTGAAT
01T071L	01T071L	GGCCCTCTATCCCAAGCAACAGC	01T071R	AAAGAAATATGGCCGTGCA	01T071E	TCCCTTGAAGCTTTGATGGCACTTC	01T071A	TGTTGAGATGTGTGTGTGTGTGAAT	01T071A	TGTTGAGATGTGTGTGTGTGTGAAT	01T071A	TGTTGAGATGTGTGTGTGTGTGAAT
01T072L	01T072L	TGTTGCTTATGATACACTTCTT	01T072R	TCTTCAATATAAAGAAATTCGGG	01T072E	GGATCTTGAATTTCTGAAATCTCTGG	01T072A	TGTTGAGATGTGTGTGTGTGTGAAT	01T072A	TGTTGAGATGTGTGTGTGTGTGAAT	01T072A	TGTTGAGATGTGTGTGTGTGTGAAT
01T074L	01T074L	ATTAGCAGTCACTTCTCTTCTGTG	01T074R	GATTTGGGCTTGATTTATAGT	01T074E	TTTCTCTGGTATTTATGTGTTTATAACA	01T074A	TGTTGAGATGTGTGTGTGTGTGAAT	01T074A	TGTTGAGATGTGTGTGTGTGTGAAT	01T074A	TGTTGAGATGTGTGTGTGTGTGAAT
01T077L	01T077L	CAAGAGAGGTCCCAACAGGAAA	01T077R	GACATATTTATTCAGACTCTCTG	01T077E	AACAGTGTCTTCTCTTCTGCTGTTT	01T077A	TGTTGAGATGTGTGTGTGTGTGAAT	01T077A	TGTTGAGATGTGTGTGTGTGTGAAT	01T077A	TGTTGAGATGTGTGTGTGTGTGAAT
01T079L	01T079L	GATGGAGGCAACAATCATCTCTT	01T079R	ACAGCATTGACAGTCAAGACTT	01T079E	GGACCTTATAGAGGTATAGTCAAGAGG	01T079A	TGTTGAGATGTGTGTGTGTGTGAAT	01T079A	TGTTGAGATGTGTGTGTGTGTGAAT	01T079A	TGTTGAGATGTGTGTGTGTGTGAAT
01T083L	01T083L	CTCTTATCTGAGAGGACCTT	01T083R	TCTGAGCTTGTGTGTGCAATTTAC	01T083E	GGCACTTACTTGGGACTTCTGATATTCGA	01T083A	TGTTGAGATGTGTGTGTGTGTGAAT	01T083A	TGTTGAGATGTGTGTGTGTGTGAAT	01T083A	TGTTGAGATGTGTGTGTGTGTGAAT
01T084L	01T084L	CAAGGCGCAAAATACTGTATGAT	01T084R	GTGAAACTCTTGGCAAATTAAC	01T084E	CTACTTATAGAGTACTAGATATGCAATTTCA	01T084A	TGTTGAGATGTGTGTGTGTGTGAAT	01T084A	TGTTGAGATGTGTGTGTGTGTGAAT	01T084A	TGTTGAGATGTGTGTGTGTGTGAAT
01T087L	01T087L	GCTTACAGACTCTCCCAAGCTGC	01T087R	TCCCAAGGCTCAAGGCGCTTAA	01T087E	CCATCTGGGCTCTCTGATCCCAAGGG	01T087A	TGTTGAGATGTGTGTGTGTGTGAAT	01T087A	TGTTGAGATGTGTGTGTGTGTGAAT	01T087A	TGTTGAGATGTGTGTGTGTGTGAAT
01T088L	01T088L	CAACCCCAAGACTCTCCAGGCAAT	01T088R	GCTGTGGCTATCTTCTTCCGCG	01T088E	TCCTTACCACCAAGCCCCCTCTT	01T088A	TGTTGAGATGTGTGTGTGTGTGAAT	01T088A	TGTTGAGATGTGTGTGTGTGTGAAT	01T088A	TGTTGAGATGTGTGTGTGTGTGAAT
01T089L	01T089L	ATTACATGCATTTAATCCAGCC	01T089R	GTTTTCAGTCTCTGTCTCCCCAC	01T089E	CAGTGAAGTGAAGTGAAGCTGAGAGCC	01T089A	TGTTGAGATGTGTGTGTGTGTGAAT	01T089A	TGTTGAGATGTGTGTGTGTGTGAAT	01T089A	TGTTGAGATGTGTGTGTGTGTGAAT

Table 11

SNP	Name	Sequence (from 5' to 3')	Left Primer	Name	Sequence (from 5' to 3')	Right Primer	Name	Sequence (from 5' to 3')	Left Primer	Name	Sequence (from 5' to 3')	Right Primer
01T090L	01T090L	CAGCATGTTTATAAAGTCTATATGGA	01T090L	01T090L	GATCCACATGGTTCACATAC	01T090E	01T090E	CTTCTCTGACACACAAATTTAAATGTAA	01T090A	01T090A	TTACAATTTTAAATGTTGTGGTCAAGAAAGG	
01T091L	01T091L	ATTGGAGCCATTAACATATCTATCTAA	01T091L	01T091L	TGTTGTTTAACTCTGCAAGTAT	01T091E	01T091E	CATATAATGTTTACTCTGCGCCACAA	01T091A	01T091A	TTGTGGCCAGAGAGTAAACATTTATATG	
01T094L	01T094L	TGCAATCTCCCTCAAGGTGA	01T094L	01T094L	TACCTTGGTCTATGACAGAGTAT	01T094E	01T094E	GCAACAATGGCTCTATAGGAGAGATCC	01T094A	01T094A	GGATCTCTCTATAGCCCATGTTTGC	
01T096L	01T096L	TCACTGTCACAGAAATGTGGCTTA	01T096L	01T096L	TGGTCTCTATAGGAGCATCTAGT	01T096E	01T096E	CGACTCTCTTAATGTGGAGCTGACACT	01T096A	01T096A	AGTGTCTGAGCTCCACATTAAGGAGTGC	
01T097L	01T097L	CAGGTCCTCTTCTCTAGAGCCGC	01T097L	01T097L	AACTGCTCTACAGGCAATATAT	01T097E	01T097E	GTTCTGGTTTAACTGTGGGCTCCGCG	01T097A	01T097A	CCGAGCCACCAAGAGAACACAGAAC	
01T098L	01T098L	GGCCAAAGGTATATATCACTGTGTAG	01T098L	01T098L	ACTGAGCCACAGAGGGGAGTGAAC	01T098E	01T098E	GTACGCTCTGAACTGAGAACCCAAA	01T098A	01T098A	TTTGGGTTCCAGTTCCAGCGCTGAC	
01T099L	01T099L	CAATGCTGTCTCTCAGGGCAT	01T099L	01T099L	TGTTAATTAATCTCCAGCCATGAC	01T099E	01T099E	TGCTGCAATCTACTCTCTGCGCT	01T099A	01T099A	AGCCAGGAGTATGATGTGACGCA	
01T102L	01T102L	AGAAAGCTAGGTATCCCAAGATTA	01T102L	01T102L	CTCTCCATCACTCTCTCTGACCT	01T102E	01T102E	CTCTGCAACCCCTGGTGTGCTTTA	01T102A	01T102A	TAAAGCAAGCAGCGGTGTGCTAGG	
01T103L	01T103L	GACAGGTGATCAGGACAGCTT	01T103L	01T103L	ATCTGGCTCTTCTCTGGAGTAT	01T103E	01T103E	GGTCTTCTAAGGAGGTGATGAAATATGTC	01T103A	01T103A	GCATTAATCTCACTCTCTTATAGAAC	
01T104L	01T104L	CTGGGAGAGCTCTCTCTCAAA	01T104L	01T104L	ACACTAATACAGAAATCTGTGTA	01T104E	01T104E	GAGGATTTGCTGTTAGGATTTTATCTC	01T104A	01T104A	GAGATAAATCTTAAAGCAAACTCTC	
01T108L	01T108L	GGATGAGAGGAAACAGGCTGCT	01T108L	01T108L	GAGCCACAGATGACAGAGAC	01T108E	01T108E	CTCTGCTCTCTTATGTCCAACAAAC	01T108A	01T108A	GTTGTTTGGCATCAACAGGAGCAGAG	
01T109L	01T109L	CATTGTGCTCTCTCTCTCTCTC	01T109L	01T109L	TTCAATCTGCTATGTTCTGCG	01T109E	01T109E	GGTGAAATGAAATGTGCAAAAGCTCT	01T109A	01T109A	AGAGCTTTTCTOACCATCTCATCAAC	
01T111L	01T111L	GGCTATTGATGGAATGGTA	01T111L	01T111L	TGAATGCTATGAACCTTAC	01T111E	01T111E	CAAGCTACATCTGCAAGTCTGTACC	01T111A	01T111A	GGTACACCATCTGACAGATGATGCTG	
01T117L	01T117L	GTCTCATCTCTCTTAAAGGAA	01T117L	01T117L	CTTTTATTTTGAATGTTGTGTA	01T117E	01T117E	GCACATGATTTATTAATAGCTTTCC	01T117A	01T117A	CCATCTTAAATGTATTTACTCTCTCAAC	
01T118L	01T118L	TGCCAATCTCTCTGCAAAATCAAA	01T118L	01T118L	TTATGATGGAGATGTTGCTA	01T118E	01T118E	AATGCTCTCAACCCAGGGAAGCAG	01T118A	01T118A	CTGCTCTCTGGTTTGAAGCAAT	
01T119L	01T119L	GCCAGAGCTGATGGCAGTGAAC	01T119L	01T119L	TACAGAGGCTGCCACACTCTG	01T119E	01T119E	GGGCAATATAGCAGACCCATTC	01T119A	01T119A	GTAAAGCTATTAATCTCTCTTCTTCACTC	
01T121L	01T121L	CCTAATATCTCAATGCTTTGG	01T121L	01T121L	GGCAGATATCCCGCTCTTA	01T121E	01T121E	CTCAGGCTGGCTCTCTTATGTTCT	01T121A	01T121A	GACAACTAAAGCAGCAGCCCTGAG	
01T127L	01T127L	GAGCAGGCTGATGAGGAGATCA	01T127L	01T127L	CTGATCTGACCCAGGATGATC	01T127E	01T127E	TGGGCTGGGTTGGTGTCTGACT	01T127A	01T127A	AGGTCTAGACACCAACCCCAACCCA	
01T128L	01T128L	TCCAGGGGCTCTCTGCTGCTCT	01T128L	01T128L	GTCCAGAGGAGGAGGCTCTG	01T128E	01T128E	CATGTGAGGAGCAGAGCTCTCCATC	01T128A	01T128A	GATGGAGGCTCTCTCTCTCTCACTG	
01T129L	01T129L	ACCATAATGCAAGTATTAATCTGAC	01T129L	01T129L	GGGAGTCTGTGTCACAGCTCTAA	01T129E	01T129E	CCAGACTTCTCCCACTTAACTGTTCT	01T129A	01T129A	GACAGTTTAAAGTGGGGAAGGCTGAG	
01T131L	01T131L	CCCTGTAATTTCCAGAAATATCAG	01T131L	01T131L	CTCTCTCAGAGCTAGGGTA	01T131E	01T131E	CAGTCACTGTTACTACAGAAACCACTAA	01T131A	01T131A	TTACTGGGTGAGTAACTGCTGCTG	
01T133L	01T133L	AATCTACCAATCTGACAAAGGCT	01T133L	01T133L	CTCTTGAAGATGCTCTGTGAT	01T133E	01T133E	TAAACAAATTTACAGAAACCAACAA	01T133A	01T133A	TATCAGATTTTATTTGTTAACTGCTG	
01T135L	01T135L	TTAAAGTCTTTATGCTCTCCACC	01T135L	01T135L	AGGAATAGGATATGGTTTCTG	01T135E	01T135E	GTCACTAGCCTTTACAACTGCTT	01T135A	01T135A	TACGATTTTATTTGTTAACTGCTG	
01T137L	01T137L	AAATAGGAGACCCACTCTCTA	01T137L	01T137L	AATGGAATCCCTTACTCTGTTA	01T137E	01T137E	CTCTCCCTGAGAGGCTGCTGTA	01T137A	01T137A	TACCAGCCTCTCTCTCTCTCTCTCT	
01T138L	01T138L	GAAATGATCTCAACCAATTC	01T138L	01T138L	AATTACCACTCTCTCTCTCTCTA	01T138E	01T138E	GAGATGAGCTATACACCAACCTCT	01T138A	01T138A	GAGGCTGCTGCTCTCTCTCTCTCT	
01T145L	01T145L	GGCAGCTGGAGGTTAAGCATCTAA	01T145L	01T145L	CAGCAGAGCTGGATGATCTCTGGA	01T145E	01T145E	CTGGAACACCAATACAGAAAGGCTC	01T145A	01T145A	GGGCTCTCTCTCTCTCTCTCTCTCT	
01T146L	01T146L	ATGTTGAGCTCTCTCTCTCTGTA	01T146L	01T146L	AGGAATAGATTAATCTCTCTCTG	01T146E	01T146E	CGAGCAATGAGCTAGCTGAGGA	01T146A	01T146A	CTCTCAGCTCTCTCTCTCTCTCTCT	
01T147L	01T147L	AATATGATGAGCTAGTGAAC	01T147L	01T147L	TGCGCATATTAACATATGACT	01T147E	01T147E	CATCTGATATGATCTCTCTCTCTCT	01T147A	01T147A	TGCGCATATGAGTAACTCTCTCTCT	
01T148L	01T148L	AGGAAGAAATATAGAGAACTCTCA	01T148L	01T148L	TCCTGATATGCTCAGCTCTGACAC	01T148E	01T148E	GAAATGATTAATGCTCTCTCTCTCT	01T148A	01T148A	GACTCCATGAGCTCTCTCTCTCTCT	
01T150L	01T150L	TCAGAGAAATGCTTTGAGACCTGG	01T150L	01T150L	TTTATGAGTCACTCTCTCTCTG	01T150E	01T150E	TGTTGCCAGGCCACAGAGTGAATGG	01T150A	01T150A	CCATTACACTCTCTCTCTCTCTCTCT	
01T151L	01T151L	GTACATGGCCCTTTTATC	01T151L	01T151L	CCCAAGAGCCCAAGAGGAA	01T151E	01T151E	CCCTGTGTTGTGCAAGCTAGGGA	01T151A	01T151A	TCCTAGGCTCTCTCTCTCTCTCTCT	
01T152L	01T152L	TTCTTAAGCTCTCTATCTGCTCTG	01T152L	01T152L	ACAAATTTTAAAGCTCTCTCTGGA	01T152E	01T152E	AGAAAGCTCTCTGAAAGCACTACCTG	01T152A	01T152A	CAGGTAGCTCTCTCTCTCTCTCTCT	
01T153L	01T153L	ACTGATATGCTCTCAGGTAT	01T153L	01T153L	GAAGTCTCTCTCTCTCTCTCTG	01T153E	01T153E	TTTATATGCTCTTTATGCTATATAACATA	01T153A	01T153A	TATGTTTATATAGCTCTCTCTCTCT	
01T154L	01T154L	CCATCTCTCCCTCTTAAATA	01T154L	01T154L	TCCTCTCTCTCTCTCTCTCTCT	01T154E	01T154E	GAATATGATTAATATCTCTCTCTCT	01T154A	01T154A	CGATTTATGCTCTCTCTCTCTCTCT	
01T155L	01T155L	GGATACCTCTCTGATGAATCTCAAC	01T155L	01T155L	AGGGAATGCTGATTAATCTCTG	01T155E	01T155E	CTGATATCTCTCTCTCTCTCTCTCT	01T155A	01T155A	TTGATAGCAATAGGAATGATCTCTCT	
01T156L	01T156L	TCCTCTCTCTCTCTCTCTCTCTCT	01T156L	01T156L	GAGCAATCTATTTTGAACAACT	01T156E	01T156E	ACTGGCTCTGATGATATGATGG	01T156A	01T156A	CCATCAATCTCTCTCTCTCTCTCTCT	
01T157L	01T157L	AGCATGCTCTCTCTCTCTCTCTCT	01T157L	01T157L	TATACCATGATGATGAGAGGCT	01T157E	01T157E	GAATGATGATGATGAGAGGAGGCA	01T157A	01T157A	TGCTCTCTCTCTCTCTCTCTCTCT	
01T159L	01T159L	GTGATCTCTCTCTCTCTCTCTCT	01T159L	01T159L	ACTGAGCTCTCTGAGAGCTTT	01T159E	01T159E	CTCTAGCTCTCTCTCTCTCTCTCT	01T159A	01T159A	AACTTAATAGCTCTCTCTCTCTCTCT	
01T160L	01T160L	CCCTATGCTCTCTCTCTCTCTCT	01T160L	01T160L	ATATATTTTGAAGGCCACAG	01T160E	01T160E	AGATCAAGATTTTAACTCTCTCTCTCT	01T160A	01T160A	TTTATGATCTCTCTCTCTCTCTCTCT	
01T162L	01T162L	AATAGGTTTGAAGGAGGAAATAG	01T162L	01T162L	TCATTAATAATCTCTCTCTGCGA	01T162E	01T162E	GAACAAATATGCTCTCTCTCTCTCT	01T162A	01T162A	AGCATGATCTCTCTCTCTCTCTCTCT	
01T164L	01T164L	TAACTGTTCTCTCTCTCTCTCTCT	01T164L	01T164L	TGAGAGAGGCTCTCTCTCTCTCT	01T164E	01T164E	AGCATGATCTCTCTCTCTCTCTCTCT	01T164A	01T164A	TCGAGGCTCTCTCTCTCTCTCTCTCT	
01T166L	01T166L	CTCTCTCTCTCTCTCTCTCTCTCT	01T166L	01T166L	CACATCTCTTCTCATGTGTAT	01T166E	01T166E	ATATATGATCTCTCTCTCTCTCTCT	01T166A	01T166A	GGCATTTTGAAGGAGGATCTCTCTCT	
01T167L	01T167L	ACAAATTTTAAATGCTCTCTCTG	01T167L	01T167L	AATAGAACTCTCTCTCTCTCTCT	01T167E	01T167E	CCGCTTTTATGATTAATGTTTATG	01T167A	01T167A	CATAAACTAACTCTCTCTCTCTCTCT	
01T169L	01T169L	CATACACCTCTCTCTCTCTCTCT	01T169L	01T169L	TTGAGATCTCTCTCTCTCTCTCTCT	01T169E	01T169E	GAAGATCAAAATCTCTCTCTCTCTCT	01T169A	01T169A	TGTTATGCTCTCTCTCTCTCTCTCTCT	
01T171L	01T171L	GCAAAGGTTAAGAGAGGAAAGTGGC	01T171L	01T171L	CTGCTCTCTCTCTCTCTCTCTCTCT	01T171E	01T171E	AGAAAGCTCTCTCTCTCTCTCTCTCT	01T171A	01T171A	CAGCCATAGGTTAAAGCAAGCTCTCT	
01T172L	01T172L	ACACTCTCTCTCTCTCTCTCTCTCT	01T172L	01T172L	TCCTGATCTCTCTCTCTCTCTCTCT	01T172E	01T172E	TUCACTGACAAAGAGCAGATGCTG	01T172A	01T172A	CCCATCTCTCTCTCTCTCTCTCTCT	
01T173L	01T173L	TTATAGAGATCTCTCTCTCTCTCTCT	01T173L	01T173L	ATTAATGCTCTCTCTCTCTCTCTCT	01T173E	01T173E	CAGAAATAGGAGATCTCTCTCTCTCT	01T173A	01T173A	TCAGCAAAAGAGGTTCTCTCTCTCTCT	
01T174L	01T174L	AGAGCTCTCTCTCTCTCTCTCTCTCT	01T174L	01T174L	AATAGGCCACTCTGAAATA	01T174E	01T174E	GATCTCTCTCTCTCTCTCTCTCTCTCT	01T174A	01T174A	CTTATGAGCTCTCTCTCTCTCTCTCTCT	
01T176L	01T176L	CAGCTGAGGCTCTCTCTCTCTCTCT	01T176L	01T176L	AGTATGATTAACAGGAGCTCTCTCT	01T176E	01T176E	TGCGGAGGCTCTCTCTCTCTCTCTCT	01T176A	01T176A	CTTATGAGCTCTCTCTCTCTCTCTCTCT	
01T178L	01T178L	CTCTGTTAATAGGCTCTCTCTCTCTCT	01T178L	01T178L	CATGAGAAATGATACAGTCTCTCT	01T178E	01T178E	CTCTGTTAATAGGCTCTCTCTCTCTCT	01T178A	01T178A	CCATAATGAAACTCTCTCTCTCTCTCT	
01T180L	01T180L	TACAGATTTGAGGCTCTCTCTCTCTCT	01T180L	01T180L	ACATTAACAAAGTCTCTCTCTCTCT	01T180E	01T180E	CTTCTGAGCTCTCTCTCTCTCTCTCT	01T180A	01T180A	GGATTTCTCTCTCTCTCTCTCTCTCT	

Table 11

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Table II

SNP	Left Primer			Right Primer			Labeled Probe			Probe (from 5' to 3')		
	Name	Sequence (from 5' to 3')	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	
01T268I	01T272L	CTGAGCTCTTCCCTCCCAAT	TCATTAATATCTGCTGCTGAGTGA	01T272E	TCATTAATATCTGCTGCTGAGTGA	01T272A	ATTTACATGGAAGAGGCTTGATC	01T268G	TTGTACATGCAATGATGTCAGTG	01T270A	TTCCAGGGCATTAATGGAATGATGATG	
01T270I	01T273I	CCGAGCACTTCCCTTAATATATAGACG	TTAAATATCTGCTGCTGCTGACT	01T273E	TTAAATATCTGCTGCTGCTGACT	01T273A	GATCTTTTATCTTATTTTGGCTTCC	01T270G	TTCCAGGGCATTAATGGAATGATGATG	01T271A	GATTGCAGGCTTATTTGGCACC TGTA	
01T271I	01T274I	CAAACCTGAAGGACTCAATCT	TTCTCCCTATCTCCCTCA	01T274E	TTCTCCCTATCTCCCTCA	01T274A	TTACCTTTGTGAGCATCAATACGACGC	01T271G	GATTGCAGGCTTATTTGGCACC TGTA			
01T272I	01T277I	CGGAGCTCAGAAAGCTGCTGG	GGCAGCTGATCTTGTGCAAT	01T277E	GGCAGCTGATCTTGTGCAAT	01T277A	TTAAGGCTCTATTTGAAACAGATGCGACG					
01T273I	01T278I	GCGTAATCAAGAAATCTTAAGT	CTCTCTCGAAGTCTGTAGGAG	01T278E	CTCTCTCGAAGTCTGTAGGAG	01T278A	CTACAAATGAGATAGCATTAAGGAAG					
01T274I	01T279I	GCTTGCTGTGCTGCTCCCTGCG	GGTTTTCGCACTGGGCTCCCTGCG	01T279E	GGTTTTCGCACTGGGCTCCCTGCG	01T279A	TCCCTCTTAGGCTCAGCATGAGG					
01T275I	01T281I	ACCATCAGATCTCATAGAGAT	ACCATCAGATCTCATAGAGAT	01T281E	ACCATCAGATCTCATAGAGAT	01T281A	GCACCTCTAGGCTCAGCATGAGG					
01T276I	01T282I	AGGATGCCATCTATCAATTC	AGGATGCCATCTATCAATTC	01T282E	AGGATGCCATCTATCAATTC	01T282A	GCACCTCTAGGCTCAGCATGAGG					
01T277I	01T283I	AGCGGTGTGGTCTGGGCAAGAACG	GTAAAGCAATCAAGCAATTAAGACT	01T283E	GTAAAGCAATCAAGCAATTAAGACT	01T283A	CAGCATCTAGGCTCAGCATGAGG					
01T278I	01T284I	GTAAAGCAATCAAGCAATTAAGACT	GTAAAGCAATCAAGCAATTAAGACT	01T284E	GTAAAGCAATCAAGCAATTAAGACT	01T284A	GCACCTCTAGGCTCAGCATGAGG					
01T279I	01T285I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T285E	GGTTTACGATCTTCTCAAA	01T285A	TGGTCTCTAGGCTTATTTAGTATGCTGTC					
01T280I	01T286I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T286E	GGTTTACGATCTTCTCAAA	01T286A	AATATGTTGTGAAAGTGCTGAGACGACG					
01T281I	01T287I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T287E	GGTTTACGATCTTCTCAAA	01T287A	CTCTGCTCTAGGCTTATTTCTTCTCTG					
01T282I	01T288I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T288E	GGTTTACGATCTTCTCAAA	01T288A	AATCTTATTTTAAATCTTCTTCTTATTTAT					
01T283I	01T289I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T289E	GGTTTACGATCTTCTCAAA	01T289A	TTAAGATATATTTTATTCGAAATGGAATATG					
01T284I	01T290I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T290E	GGTTTACGATCTTCTCAAA	01T290A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T285I	01T291I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T291E	GGTTTACGATCTTCTCAAA	01T291A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T286I	01T292I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T292E	GGTTTACGATCTTCTCAAA	01T292A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T287I	01T293I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T293E	GGTTTACGATCTTCTCAAA	01T293A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T288I	01T294I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T294E	GGTTTACGATCTTCTCAAA	01T294A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T289I	01T295I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T295E	GGTTTACGATCTTCTCAAA	01T295A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T290I	01T296I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T296E	GGTTTACGATCTTCTCAAA	01T296A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T291I	01T297I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T297E	GGTTTACGATCTTCTCAAA	01T297A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T292I	01T298I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T298E	GGTTTACGATCTTCTCAAA	01T298A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T293I	01T299I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T299E	GGTTTACGATCTTCTCAAA	01T299A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T294I	01T300I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T300E	GGTTTACGATCTTCTCAAA	01T300A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T295I	01T301I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T301E	GGTTTACGATCTTCTCAAA	01T301A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T296I	01T302I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T302E	GGTTTACGATCTTCTCAAA	01T302A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T297I	01T303I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T303E	GGTTTACGATCTTCTCAAA	01T303A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T298I	01T304I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T304E	GGTTTACGATCTTCTCAAA	01T304A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T299I	01T305I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T305E	GGTTTACGATCTTCTCAAA	01T305A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T300I	01T306I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T306E	GGTTTACGATCTTCTCAAA	01T306A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T301I	01T307I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T307E	GGTTTACGATCTTCTCAAA	01T307A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T302I	01T308I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T308E	GGTTTACGATCTTCTCAAA	01T308A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T303I	01T309I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T309E	GGTTTACGATCTTCTCAAA	01T309A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T304I	01T310I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T310E	GGTTTACGATCTTCTCAAA	01T310A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T305I	01T311I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T311E	GGTTTACGATCTTCTCAAA	01T311A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T306I	01T312I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T312E	GGTTTACGATCTTCTCAAA	01T312A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T307I	01T313I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T313E	GGTTTACGATCTTCTCAAA	01T313A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T308I	01T314I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T314E	GGTTTACGATCTTCTCAAA	01T314A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T309I	01T315I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T315E	GGTTTACGATCTTCTCAAA	01T315A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T310I	01T316I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T316E	GGTTTACGATCTTCTCAAA	01T316A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T311I	01T317I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T317E	GGTTTACGATCTTCTCAAA	01T317A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T312I	01T318I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T318E	GGTTTACGATCTTCTCAAA	01T318A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T313I	01T319I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T319E	GGTTTACGATCTTCTCAAA	01T319A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T314I	01T320I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T320E	GGTTTACGATCTTCTCAAA	01T320A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T315I	01T321I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T321E	GGTTTACGATCTTCTCAAA	01T321A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T316I	01T322I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T322E	GGTTTACGATCTTCTCAAA	01T322A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T317I	01T323I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T323E	GGTTTACGATCTTCTCAAA	01T323A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T318I	01T324I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T324E	GGTTTACGATCTTCTCAAA	01T324A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T319I	01T325I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T325E	GGTTTACGATCTTCTCAAA	01T325A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T320I	01T326I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T326E	GGTTTACGATCTTCTCAAA	01T326A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T321I	01T327I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T327E	GGTTTACGATCTTCTCAAA	01T327A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T322I	01T328I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T328E	GGTTTACGATCTTCTCAAA	01T328A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T323I	01T329I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T329E	GGTTTACGATCTTCTCAAA	01T329A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T324I	01T330I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T330E	GGTTTACGATCTTCTCAAA	01T330A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T325I	01T331I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T331E	GGTTTACGATCTTCTCAAA	01T331A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T326I	01T332I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T332E	GGTTTACGATCTTCTCAAA	01T332A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T327I	01T333I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T333E	GGTTTACGATCTTCTCAAA	01T333A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T328I	01T334I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T334E	GGTTTACGATCTTCTCAAA	01T334A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T329I	01T335I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T335E	GGTTTACGATCTTCTCAAA	01T335A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T330I	01T336I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T336E	GGTTTACGATCTTCTCAAA	01T336A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T331I	01T337I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T337E	GGTTTACGATCTTCTCAAA	01T337A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T332I	01T338I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T338E	GGTTTACGATCTTCTCAAA	01T338A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T333I	01T339I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T339E	GGTTTACGATCTTCTCAAA	01T339A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T334I	01T340I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T340E	GGTTTACGATCTTCTCAAA	01T340A	TAAGGATATATTTTATTCGAAATGGAATATG					
01T335I	01T341I	GGTTTACGATCTTCTCAAA	GGTTTACGATCTTCTCAAA	01T341E	GGTTTACGATCTTCTCAAA	01T341A	TAAGGATATATTTTATTCGAAATGGAATATG					

Table 11

SNP	Name	Sequence (from 5' to 3')	Left Primer	Name	Sequence (from 5' to 3')	Right Primer	Name	Sequence (from 5' to 3')	Right Primer
01T342L	01T342L	TTGGAGGATATCATCTTGGACTCTCT	01T342R	01T342R	AAATGAAATCTTACGGGCGCA	01T342L	01T342L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T342L
01T343L	01T343L	AGTTTCAGAGTTCAGCTTCA	01T343R	01T343R	CAATGATATCTTACGGGCGCA	01T343L	01T343L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T343L
01T344L	01T344L	TTTGAAGACATGACGCGCAAAACT	01T344R	01T344R	CACCAATGCTTCTTCTTCTCTG	01T344L	01T344L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T344L
01T346L	01T346L	ATTACATGGAAGCGGAAATATGAT	01T346R	01T346R	GTGGGTGGGAGTGTAGTGTGG	01T346L	01T346L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T346L
01T349L	01T349L	GTGATCTCTTCAAAATGATGATCA	01T349R	01T349R	AAATGAAATCTTACGGGCGCA	01T349L	01T349L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T349L
01T351L	01T351L	GCACATAAAGAAACAGAGCGCGGA	01T351R	01T351R	CACTGTCGGGCGCACTGTAG	01T351L	01T351L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T351L
01T353L	01T353L	AAATGCTCTGGAGAGCCCTCA	01T353R	01T353R	GAATCTATCAACGAGGAGGTTA	01T353L	01T353L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T353L
01T354L	01T354L	CTCTCTGAGGCTGACTGGC	01T354R	01T354R	CAGTATGCTTCTTCTTCTTCT	01T354L	01T354L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T354L
01T355L	01T355L	AGGTCTCATCTCTCTCTGGA	01T355R	01T355R	GGCCCACTAATGAGGCTAAT	01T355L	01T355L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T355L
01T356L	01T356L	TGTAGTCACTCTATCTCTCAAT	01T356R	01T356R	AACTTTACAAATCTGGAATC	01T356L	01T356L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T356L
01T357L	01T357L	GAACAGATGATAGCTGTGGGTA	01T357R	01T357R	AACTTACAGATGCAATAGGCTT	01T357L	01T357L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T357L
01T358L	01T358L	TTTCACTGATCTCTCTGCTTGA	01T358R	01T358R	AACAGGATATTAATCACTGAT	01T358L	01T358L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T358L
01T359L	01T359L	AAACATCTCTGCAATATGTC	01T359R	01T359R	TGTCCACATTTACTATTCAG	01T359L	01T359L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T359L
01T360L	01T360L	GCOCAGGAAATACAGAGGCTTA	01T360R	01T360R	TTTCTTCTCTTATCAGCAAC	01T360L	01T360L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T360L
01T361L	01T361L	GCTGAGGCTCTGCTGCTGTC	01T361R	01T361R	TTTCTTCTCTTATCAGCAAC	01T361L	01T361L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T361L
01T362L	01T362L	GAATCTGGAATGATTTGCACTA	01T362R	01T362R	TGAGTGTCTTACTCTCACT	01T362L	01T362L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T362L
01T363L	01T363L	TCATATATGCACTATGCTCTTA	01T363R	01T363R	AAACAAACAAACAAATGCTCC	01T363L	01T363L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T363L
01T364L	01T364L	AAATGCTCTGTAATACAGCATCT	01T364R	01T364R	TCGGGCTGTATTAAGCAAAATA	01T364L	01T364L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T364L
01T365L	01T365L	TGTAACTCTTAATTTGGGCT	01T365R	01T365R	GCACATCTGATGATGCTGAA	01T365L	01T365L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T365L
01T366L	01T366L	CTCTCATCTCACTTAAGGTA	01T366R	01T366R	TAGTCTCTTATCAGCTCAGT	01T366L	01T366L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T366L
01T367L	01T367L	GCCTCATCTCACTTAAGGTA	01T367R	01T367R	ACTGAGGCCAATCTCTATGTA	01T367L	01T367L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T367L
01T368L	01T368L	GCCTCATCTCACTTAAGGTA	01T368R	01T368R	CTGAGGCCAATCTCTATGTA	01T368L	01T368L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T368L
01T369L	01T369L	GCCTCATCTCACTTAAGGTA	01T369R	01T369R	CTGAGGCCAATCTCTATGTA	01T369L	01T369L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T369L
01T370L	01T370L	GCCTCATCTCACTTAAGGTA	01T370R	01T370R	CTGAGGCCAATCTCTATGTA	01T370L	01T370L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T370L
01T371L	01T371L	GCCTCATCTCACTTAAGGTA	01T371R	01T371R	CTGAGGCCAATCTCTATGTA	01T371L	01T371L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T371L
01T372L	01T372L	GCCTCATCTCACTTAAGGTA	01T372R	01T372R	CTGAGGCCAATCTCTATGTA	01T372L	01T372L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T372L
01T373L	01T373L	GCCTCATCTCACTTAAGGTA	01T373R	01T373R	CTGAGGCCAATCTCTATGTA	01T373L	01T373L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T373L
01T374L	01T374L	GCCTCATCTCACTTAAGGTA	01T374R	01T374R	CTGAGGCCAATCTCTATGTA	01T374L	01T374L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T374L
01T375L	01T375L	GCCTCATCTCACTTAAGGTA	01T375R	01T375R	CTGAGGCCAATCTCTATGTA	01T375L	01T375L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T375L
01T376L	01T376L	GCCTCATCTCACTTAAGGTA	01T376R	01T376R	CTGAGGCCAATCTCTATGTA	01T376L	01T376L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T376L
01T377L	01T377L	GCCTCATCTCACTTAAGGTA	01T377R	01T377R	CTGAGGCCAATCTCTATGTA	01T377L	01T377L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T377L
01T378L	01T378L	GCCTCATCTCACTTAAGGTA	01T378R	01T378R	CTGAGGCCAATCTCTATGTA	01T378L	01T378L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T378L
01T379L	01T379L	GCCTCATCTCACTTAAGGTA	01T379R	01T379R	CTGAGGCCAATCTCTATGTA	01T379L	01T379L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T379L
01T380L	01T380L	GCCTCATCTCACTTAAGGTA	01T380R	01T380R	CTGAGGCCAATCTCTATGTA	01T380L	01T380L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T380L
01T381L	01T381L	GCCTCATCTCACTTAAGGTA	01T381R	01T381R	CTGAGGCCAATCTCTATGTA	01T381L	01T381L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T381L
01T382L	01T382L	GCCTCATCTCACTTAAGGTA	01T382R	01T382R	CTGAGGCCAATCTCTATGTA	01T382L	01T382L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T382L
01T383L	01T383L	GCCTCATCTCACTTAAGGTA	01T383R	01T383R	CTGAGGCCAATCTCTATGTA	01T383L	01T383L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T383L
01T384L	01T384L	GCCTCATCTCACTTAAGGTA	01T384R	01T384R	CTGAGGCCAATCTCTATGTA	01T384L	01T384L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T384L
01T385L	01T385L	GCCTCATCTCACTTAAGGTA	01T385R	01T385R	CTGAGGCCAATCTCTATGTA	01T385L	01T385L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T385L
01T386L	01T386L	GCCTCATCTCACTTAAGGTA	01T386R	01T386R	CTGAGGCCAATCTCTATGTA	01T386L	01T386L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T386L
01T387L	01T387L	GCCTCATCTCACTTAAGGTA	01T387R	01T387R	CTGAGGCCAATCTCTATGTA	01T387L	01T387L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T387L
01T388L	01T388L	GCCTCATCTCACTTAAGGTA	01T388R	01T388R	CTGAGGCCAATCTCTATGTA	01T388L	01T388L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T388L
01T389L	01T389L	GCCTCATCTCACTTAAGGTA	01T389R	01T389R	CTGAGGCCAATCTCTATGTA	01T389L	01T389L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T389L
01T390L	01T390L	GCCTCATCTCACTTAAGGTA	01T390R	01T390R	CTGAGGCCAATCTCTATGTA	01T390L	01T390L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T390L
01T391L	01T391L	GCCTCATCTCACTTAAGGTA	01T391R	01T391R	CTGAGGCCAATCTCTATGTA	01T391L	01T391L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T391L
01T392L	01T392L	GCCTCATCTCACTTAAGGTA	01T392R	01T392R	CTGAGGCCAATCTCTATGTA	01T392L	01T392L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T392L
01T393L	01T393L	GCCTCATCTCACTTAAGGTA	01T393R	01T393R	CTGAGGCCAATCTCTATGTA	01T393L	01T393L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T393L
01T394L	01T394L	GCCTCATCTCACTTAAGGTA	01T394R	01T394R	CTGAGGCCAATCTCTATGTA	01T394L	01T394L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T394L
01T395L	01T395L	GCCTCATCTCACTTAAGGTA	01T395R	01T395R	CTGAGGCCAATCTCTATGTA	01T395L	01T395L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T395L
01T396L	01T396L	GCCTCATCTCACTTAAGGTA	01T396R	01T396R	CTGAGGCCAATCTCTATGTA	01T396L	01T396L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T396L
01T397L	01T397L	GCCTCATCTCACTTAAGGTA	01T397R	01T397R	CTGAGGCCAATCTCTATGTA	01T397L	01T397L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T397L
01T398L	01T398L	GCCTCATCTCACTTAAGGTA	01T398R	01T398R	CTGAGGCCAATCTCTATGTA	01T398L	01T398L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T398L
01T399L	01T399L	GCCTCATCTCACTTAAGGTA	01T399R	01T399R	CTGAGGCCAATCTCTATGTA	01T399L	01T399L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T399L
01T400L	01T400L	GCCTCATCTCACTTAAGGTA	01T400R	01T400R	CTGAGGCCAATCTCTATGTA	01T400L	01T400L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T400L
01T401L	01T401L	GCCTCATCTCACTTAAGGTA	01T401R	01T401R	CTGAGGCCAATCTCTATGTA	01T401L	01T401L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T401L
01T402L	01T402L	GCCTCATCTCACTTAAGGTA	01T402R	01T402R	CTGAGGCCAATCTCTATGTA	01T402L	01T402L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T402L
01T403L	01T403L	GCCTCATCTCACTTAAGGTA	01T403R	01T403R	CTGAGGCCAATCTCTATGTA	01T403L	01T403L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T403L
01T404L	01T404L	GCCTCATCTCACTTAAGGTA	01T404R	01T404R	CTGAGGCCAATCTCTATGTA	01T404L	01T404L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T404L
01T405L	01T405L	GCCTCATCTCACTTAAGGTA	01T405R	01T405R	CTGAGGCCAATCTCTATGTA	01T405L	01T405L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T405L
01T406L	01T406L	GCCTCATCTCACTTAAGGTA	01T406R	01T406R	CTGAGGCCAATCTCTATGTA	01T406L	01T406L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T406L
01T407L	01T407L	GCCTCATCTCACTTAAGGTA	01T407R	01T407R	CTGAGGCCAATCTCTATGTA	01T407L	01T407L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T407L
01T408L	01T408L	GCCTCATCTCACTTAAGGTA	01T408R	01T408R	CTGAGGCCAATCTCTATGTA	01T408L	01T408L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T408L
01T409L	01T409L	GCCTCATCTCACTTAAGGTA	01T409R	01T409R	CTGAGGCCAATCTCTATGTA	01T409L	01T409L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T409L
01T410L	01T410L	GCCTCATCTCACTTAAGGTA	01T410R	01T410R	CTGAGGCCAATCTCTATGTA	01T410L	01T410L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T410L
01T411L	01T411L	GCCTCATCTCACTTAAGGTA	01T411R	01T411R	CTGAGGCCAATCTCTATGTA	01T411L	01T411L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T411L
01T412L	01T412L	GCCTCATCTCACTTAAGGTA	01T412R	01T412R	CTGAGGCCAATCTCTATGTA	01T412L	01T412L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T412L
01T413L	01T413L	GCCTCATCTCACTTAAGGTA	01T413R	01T413R	CTGAGGCCAATCTCTATGTA	01T413L	01T413L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T413L
01T414L	01T414L	GCCTCATCTCACTTAAGGTA	01T414R	01T414R	CTGAGGCCAATCTCTATGTA	01T414L	01T414L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T414L
01T415L	01T415L	GCCTCATCTCACTTAAGGTA	01T415R	01T415R	CTGAGGCCAATCTCTATGTA	01T415L	01T415L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T415L
01T416L	01T416L	GCCTCATCTCACTTAAGGTA	01T416R	01T416R	CTGAGGCCAATCTCTATGTA	01T416L	01T416L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T416L
01T417L	01T417L	GCCTCATCTCACTTAAGGTA	01T417R	01T417R	CTGAGGCCAATCTCTATGTA	01T417L	01T417L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T417L
01T418L	01T418L	GCCTCATCTCACTTAAGGTA	01T418R	01T418R	CTGAGGCCAATCTCTATGTA	01T418L	01T418L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T418L
01T419L	01T419L	GCCTCATCTCACTTAAGGTA	01T419R	01T419R	CTGAGGCCAATCTCTATGTA	01T419L	01T419L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T419L
01T420L	01T420L	GCCTCATCTCACTTAAGGTA	01T420R	01T420R	CTGAGGCCAATCTCTATGTA	01T420L	01T420L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T420L
01T421L	01T421L	GCCTCATCTCACTTAAGGTA	01T421R	01T421R	CTGAGGCCAATCTCTATGTA	01T421L	01T421L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T421L
01T422L	01T422L	GCCTCATCTCACTTAAGGTA	01T422R	01T422R	CTGAGGCCAATCTCTATGTA	01T422L	01T422L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T422L
01T423L	01T423L	GCCTCATCTCACTTAAGGTA	01T423R	01T423R	CTGAGGCCAATCTCTATGTA	01T423L	01T423L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T423L
01T424L	01T424L	GCCTCATCTCACTTAAGGTA	01T424R	01T424R	CTGAGGCCAATCTCTATGTA	01T424L	01T424L	GTCAAGTGAAGAAAGTGGCAAACTCTGT	01T424L

[illegible]

Table 11

SNP	Name	Sequence (from 5' to 3')	Left Primer	Name	Sequence (from 5' to 3')	Right Primer	Name	Sequence (from 5' to 3')	Probe on Slide
16-0121	16-0121	GCTGAGGCTCAGATGATGAT		16-0122	TGCTCATCATCTCTGTCCTGA		16-012A	AGGAGAGCAGATGCTCCACAAAGACAGGT	
16-0131	16-0131	CCCTTCTCTCCCAATGGA		16-0132	CATCCCAACATCAACAGAGTCG		16-013A	AGCCACACCTCGGTGCGCAGAGTCT	
16-0141	16-0141	ACATCTGTGAGCTTGACAA		16-0142	AGTGGTCCAGGGTTTGG		16-014A	TAGTGTATGACAGATATTTTCACTGCCCT	
16-0161	16-0161	CATCAGCTCAGAGCTGGAG		16-0162	GTGAGTGTCTCTCTGTGTGA		16-016A	CACAUGGTAGCTCTGAGTTAGGTGTCA	
16-0171	16-0171	AAACCCAGACAGCTGAAGCGGC		16-0172	AGCTGTGGTCCCATATGGGTAA		16-017A	AGCAGGATGCTCTGCTCCCGACAC	
16-0181	16-0181	TAATCCAAACACATAGAGGCTAA		16-0182	TTAGTGACGACATAGAGCG		16-018A	GAATTAAGATATCATCTGCTACGACCTT	
16-0201	16-0201	TACTGCACAGCCCATCTA		16-0202	AACGAGATGAGCTGCTTAATAGTA		16-020A	CCTGCGCTGGAAGAGAGCCAGGTCTAGAA	
16-0211	16-0211	TCAGAGAGCCCTTATGCGC		16-0212	TTGCTCTGATCTACTGTGAGAC		16-021A	TTTCCACAAAGACAGGTCACTTTTCCACCA	
16-0221	16-0221	GGATGATGTTTCCCAAC		16-0222	CATCAGCTGCTATCTAAATGCT		16-022A	AGACTATATATACCTCCGAGATACATGTT	
16-0231	16-0231	TCTCTCTCTGACCTCTGCGAT		16-0232	TTGTGTGCAAAATTTGGCTGTGA		16-023A	AGGTGCTGAGAAAGGGGCTGCTATATA	
16-0241	16-0241	AGCGGTGCTCTCTCTCATG		16-0242	GGAGCGCAACCTCTCTCTTAC		16-024A	GTATCCACAAACATATCACTCTCAATAAT	
16-0251	16-0251	ATCTGTCTCTCTGACAC		16-0252	GTGAATGAGGCTTGGTGCTGACA		16-025A	AGCTGGGTGGAAGGCTGCTGCAAGTG	
16-0261	16-0261	TCTCCACATTAAGGCAAGTG		16-0262	TGGAATGATGAGGGGTAGTG		16-026A	CCCTGGAATCGCAAGAGGCGACATC	
16-0281	16-0281	TGCGACAGCGCTTACCTAGT		16-0282	CTCTGCTGATGAGCTGGAGCTGAGGTT		16-028A	AACCTTCAGCTCATCGCTCCATCAGGAC	
16-0311	16-0311	TCCTCTCTAATGTCTATG		16-0312	CAAGTGGAGAAAGAAATCT		16-031A	CCTGACACACCCAGATGCAATCTCTGG	
16-0321	16-0321	TGAGGAGTCTGTGAAATCT		16-0322	TTATACATATCAGAGCGGAAA		16-032A	CCTGCTTAAAGAGAGAACTGGAATTT	
16-0331	16-0331	GCATCTCTAGAAATGCGAT		16-0332	TGGAGAAATTTGCTCAAT		16-033A	TAGCCACATAGAAATGAAAGCTCTGCTCC	
16-0351	16-0351	CACGCTCAACAGCTGTCTCCCT		16-0352	CTCTGTGAGCTGTTAGAAC		16-035A	CTTGTCTCAGCAATTTGTTTTTCCCCAC	
16-0371	16-0371	ATGGCGCATGCGCTCTTTAC		16-0372	GGGCAACAAGAAAGAACTGCT		16-037A	TTGCGAGAGGGGCGACAAACAGCAGC	
16-0381	16-0381	ATCTCCCAATCTGGGTTCG		16-0382	GAATGAAGTCCCGAGGTA		16-038A	TCCAGAGCAACAGAGCTTCCAGTGGTGG	
16-0391	16-0391	TGCGCTCTCTGAGTTTACAGTCTG		16-0392	TAATTTCTTCATCTGCTGAT		16-039A	CAGATAAGTAATAAGCGTTTCAATATACTA	
16-0401	16-0401	GATCTACAGGTTCTCTCGG		16-0402	ATGATGATGTTGTTCTCAG		16-040A	ATACCATCATCTATATCTCAGCCATCA	
16-0411	16-0411	GGTGTGCTCTTAATTAATC		16-0412	AATTCACATCTCTTAATGACCT		16-041A	AAAGCTCTCTAGTAAGTCTGAGAGTGGGA	
16-0441	16-0441	GCATATCTTACAGCTTAAAGAC		16-0442	CGAGTAGCTCTCTGATTTTAC		16-044A	TATACAGCATATGCGATCCCTCAAGGDA	
16-0451	16-0451	AGCGCGGCTCTCTGACGACGA		16-0452	CTCTCTCTCTTATGATTTAT		16-045A	TGGTGTCTGATACGATGAGTTTGTCTGT	
16-0461	16-0461	TCCGAGCTACTGGGAGGCTA		16-0462	ATCTCTTTTAAATTTCCAGATGG		16-046A	CGAAGCTCTTCAACCCACCAAGCTCTGG	
16-0471	16-0471	AGCTACTGATGACCTGGGTCCG		16-0472	AATGCTATAGAGAAAGACCGC		16-047A	CTGATGAGAGCCCTTGAACCTTCGGCG	
16-0481	16-0481	ATCAATCTCTCTGTTTATGA		16-0482	CTTAAACCATATGTTGACCTTAC		16-048A	CTGACATATTAATAGTATGGAAGTATGAC	
16-0491	16-0491	ATCAATCTCTCTGTTTATGA		16-0492	ATCTCTTAAATTTCCAGATGG		16-049A	TAATGGAAGAAATGTCGCAAGGTCTTAA	
16-0511	16-0511	AACTGCGAGGTTGCGAT		16-0512	CAAGCTCCCATTAAGCCCATCTT		16-051A	AACTCTCAGCAGCTATAGTGTAGTGGG	
16-0531	16-0531	CTCTCCCACTAGACAGGAC		16-0532	GAATCTCCACAGCTCTGAC		16-053A	GGATTTGACATGAGCGCAAGAGCTCCGC	
16-0541	16-0541	CATCTTGAATGACAGGTTGGT		16-0542	AGAGGAGGCTTGAAGAGCGGCG		16-054A	CTGCGCTTGTGATTAATGATGAGTGTAG	
16-0551	16-0551	CTGCGAGTCCAGAGATGGTTA		16-0552	CCAGCTCCCATTAAGCCCATCTT		16-055A	TGCGACCAAGGCTAATCTCAGGGGTC	
16-0561	16-0561	TGAGGTTCTGTGCTTTCTTCC		16-0562	AGTGGGCTTAAAGGTGACAT		16-056A	CTGCGCTTGTGATTAATGATGAGTGTAG	
16-0581	16-0581	CTTAGCTCAGAGGTGCTATCTA		16-0582	TCCACATCTCTGAGGTTTGG		16-058A	AGCCAAAGCTCGAGGTCTATACAGAGTT	
16-0591	16-0591	AGCCAACTTAATTTTA		16-0592	TTCTCATAGCTCAGACCCCGC		16-059A	GCTGCTTTTGTGCTGCTGCTGCTCTCT	
16-0611	16-0611	GAAGCAATGGCCAAAGAAACAGTTA		16-0612	GAACACAGCTGCTGCTGAC		16-061A	GTTCGCTTTTGTGCTGCTGCTGCTCTCT	
16-0621	16-0621	ACTTCTTCTGCTGCTCTCT		16-0622	ATCCGACCCGCTGACCCGAT		16-062A	ATONAGGUCATGCTGCTGCTGCTGCTCT	
16-0631	16-0631	ACTTACAGCTGGGGTCTGGGCG		16-0632	TGTCTCTGAGGAGCATCTGGAG		16-063A	GGCGGCTTAACTAGTGGGCTCTCTCT	
16-0641	16-0641	ATAAGTGAATCTCCGTACGAT		16-0642	TGTCTCTGAGGAGCATCTGGAG		16-064A	TOTTCAGCCCACTGATGCTGCTCTCT	
16-0651	16-0651	TTCTCTCTAAATATATGCGCTC		16-0652	AGGAAAGCCACTCTCTCCAC		16-065A	GATTTCTCAAGCCCAAGAGGAGGGG	
16-0661	16-0661	GTAGCTTCTCCAGAGGCTCTTA		16-0662	AAGTGCACATTTCTAGATCT		16-066A	GTATGCTGACGCTACTAGAGTGGGAG	
16-0671	16-0671	CCACTTCTCTCTGCTCTCA		16-0672	GAATAGGCTGAGTGGCCACACG		16-067A	AGCTGCTCTGACAGGCTCTCACACC	
16-0681	16-0681	ACCAGCTTTTCCGAGGCTTA		16-0682	AGCAGCCTCTGCTGGAATA		16-068A	TATGCTGCTGAGGCTCTGCTGCTCTCT	
16-0691	16-0691	CCAAATGACATGCTGCTGAA		16-0692	CATGGGCAATGCTTACGAT		16-069A	GGGTGGGAGGCTGAGGAGGAGCTGAG	
16-0701	16-0701	CTCCAGGCTCTCTGCTCT		16-0702	GATCTGGTTTGTGCTGCTGCTGCT		16-070A	TCACCCAAAGGCTCTGCTCTCTCTCTCT	
16-0711	16-0711	ACATCTATCTCTCTTATCTAA		16-0712	TGGAAGAGGCTCTGCTGCTGCTGCT		16-071A	CTAACTCTGGGCTCTTCTGCAAACTCTCT	
16-0721	16-0721	ACATGTTCTCTCTCTCTCT		16-0722	GTGAGAGGCTCTGCTGCTGCTGCT		16-072A	CACTGCTCTTAAGGGAATTTTGGAGATGCT	
16-0731	16-0731	ACTGACGCTGACAGATGACA		16-0732	GTGAGAGGCTCTGCTGCTGCTGCT		16-073A	CACTGCTCTTAAGGGAATTTTGGAGATGCT	

Left Primer			Right Primer			Probe on Slide		
Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	
16-0751L	TTTAACTCAGTCTGCTGTTTGTGTTA	16-0751R	GTGTCTGCCATACAGUQTAT	16-0751L	TTAAGTTGTTATGCTGTCAATTGCTATG	16-0751A	CAATGCAATTAACAGCAATACCAACTTAA	
16-0761L	TGACTCTGCTGCTGGGTTGAGATTTCT	16-0761R	TTTCTCAGAAATACCAATCCCTG	16-0761L	CTGCTCTTCTCAGACCTCTCATCTGCACC	16-0761A	GGGTGCACAGATAGAGGCTGTAAGAACGAG	
16-0771L	CTTGGCGGAGGCTGTGCTATCATCT	16-0771R	TCCAGAGCAATTTGCTCTTACCA	16-0771L	ACAGAACTTAGATCTGAGCTTCTCGGCACC	16-0771A	CGTGCAGAGAGCTCAGATCAAGTCTGCTGT	
16-0791L	TATGAATATGAAATACAGCAT	16-0791R	TTAGAAGTTTGGATGACAGAAAGGCG	16-0791L	AGAGTGAATGCTTCTCAGTGAAGAAATCA	16-0791A	TGATCTCTTCTCAGTGAAGCTCACTCTCT	
16-0801L	ATCAAAAGGCTCAGTACAGCAATCT	16-0801R	CTCCGCGCAGGAACCAAGATTTCT	16-0801L	CATCAGCAGTATCATGCTGCTGAGTCAAGGT	16-0801A	ACCCTGACTCAGGCAATGATCACTGCTGATG	
16-0811L	ACGCTTACAGCTCTGGTCAAAACCG	16-0811R	CATTTAGCTCTCTTGGCAGAAC	16-0811L	TGTGGAAGCGCCGAGATGATAGGCA	16-0811A	TGCTCTACTCTCGCGGCTCTCTCCACA	
16-0821L	AAATCAGGTTTCTACAAACG	16-0821R	CTGTGCTTAAAGAGGCTC	16-0821L	CAGCTTGAATTTGCTGCTCGCGTGAAGCG	16-0821A	CGCTACCGGAGCAGCAATATACAGAGCTG	
Left Primer			Right Primer			Probe on Slide		
Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	
16-0831L	AGGAAATCAGAGCTGAAAT	16-0831R	GCTCAGCTCAGCTGAGATTC	16-0831L	TAGATTTGGACAAATATCTTGTCTTTTAG	16-0831A	CTAGAAAGAGCAAGTATTTGTCCCAATCTTA	
16-0861L	TTGAGCTGGGGGCTGCTGCTGCTG	16-0861R	ACTCAGACAGCTCTCTG	16-0861L	GAGGTGCTGCTGCTGCTGCTGCTGCTG	16-0861A	CGCTGGGACATCTCAGGCTGCACTTC	
16-0871L	GCAGGGAAGAGTGTATCAAT	16-0871R	CAGGTGCTGCTGCTTACGAT	16-0871L	CATGGGTGGAAGGGGACAGGCTCTC	16-0871A	GGAGGCTGTGCTGCTTCTACCCCATG	
16-0881L	AGTCCGAGGATGTAGGTGATC	16-0881R	GGAATGCTGCTGCTACTGTG	16-0881L	GACCTCTAGCTTCTTCTCCCACTAGCAT	16-0881A	CCACCCAGGCTCCCTCCAGGAGGCTC	
16-0891L	CATGACACTGATGAGGCTG	16-0891R	TTTGGAGCTGCTGCTGCTGCTG	16-0891L	AGCTCTAGCTTCTTCTCCCACTAGCAT	16-0891A	ATCTAGTTGCTGGGCAAGAAAGCTAGAGCT	
16-0901L	GGAATGGGAGGCTGGCTCTTA	16-0901R	TCAGGCTGCAAGAGGAGCACTC	16-0901L	GAACCTCAGCTGCTGCTGCTGCTGCTG	16-0901A	GTGAGGCTCACTCAAGTCTGCTGCTGCTG	
16-0911L	TTTGGGCAAGCAACTGCG	16-0911R	GAAATTTGCTACTCAGGACCTT	16-0911L	TATTTGCGGCTGGGCAATATTAATCA	16-0911A	TCCTCTTCTATCCCAAGCTTACAGTGT	
16-0921L	GTTCATGTCTCAATTAATCTGGTTAC	16-0921R	CCCTTTTCAAGACAGCTTA	16-0921L	CAGCTTATCAATCACTGATGATGATGCA	16-0921A	TGATTAATATGCTGCTGCTGCTGCTGCTG	
16-0931L	CTCAACCTTCAAAATCAAGT	16-0931R	AGTTATTTTCAACCAAAAT	16-0931L	TTTGTCTTGACTTCTCAATTTGAGAGGGA	16-0931A	TGCACTATCACTGATTTGAATGAAGGCTG	
16-0941L	ATCCAGAAATATGACACAGCTTA	16-0941R	GTCTGTTGCTCTGATTAAGT	16-0941L	AAGTTTACACTCTTCAATCTGAGAGGGA	16-0941A	TCCCTCTCAGAAATGGAAGTCAACAGCAA	
16-0951L	AGGGGAAGGAAAGATATATG	16-0951R	TCAGCAGAGTGCAGAGATGGGG	16-0951L	AGTTTACACTCTTCAATCTGAGAGGGA	16-0951A	TCCCTCTCAGAAATGGAAGTCAACAGCAA	
16-0961L	TGCTTCCAGCTGGGCTCAG	16-0961R	TCAGCAGAGTGCAGAGATGGGG	16-0961L	AGTTTACACTCTTCAATCTGAGAGGGA	16-0961A	TCCCTCTCAGAAATGGAAGTCAACAGCAA	
16-0971L	AGTTGTAGATGGCCATGCTGTA	16-0971R	TGCTCTGCTGCTCTCTG	16-0971L	AGTTTACACTCTTCAATCTGAGAGGGA	16-0971A	TCCCTCTCAGAAATGGAAGTCAACAGCAA	
16-0981L	AGATGTGTGCTTATCTACACGCT	16-0981R	AGTGTGCTGCTGCTGCTGCTG	16-0981L	AGTTTACACTCTTCAATCTGAGAGGGA	16-0981A	TCCCTCTCAGAAATGGAAGTCAACAGCAA	
16-0991L	GGGAAAGAAAGAAAGAAAGCTCAAT	16-0991R	GACCATGTGCTGGCAGAAAT	16-0991L	AGTTTACACTCTTCAATCTGAGAGGGA	16-0991A	TCCCTCTCAGAAATGGAAGTCAACAGCAA	
16-1001L	ATTAGGATCTCTTGTCTG	16-1001R	CATGGGCTCAGCTGCTTCTCAGCT	16-1001L	TGGCAGCTGGGCAAGGCAAGATGCTG	16-1001A	GCATTTCTGCTGCTGCTGCTGCTGCTG	
16-1011L	CACAGCTGTGCTTGTCTGCTG	16-1011R	ATTAGTACAGATTTGTTGATGTA	16-1011L	CTATTATGCTGACATCTACTGTGCTGTA	16-1011A	TCAGGCTACAGATGATGCTCAGTAAATAG	
16-1021L	GCTGTGCTGCGGAGCCAGCG	16-1021R	TGCAACTGTGAGGGCAGAA	16-1021L	CACAGCTCTGCTGCCACCAAGCA	16-1021A	TGGCTGGGTGGCAGCAGGCTGCTG	
16-1031L	CACCTCTGATTTATGTGAG	16-1031R	TTTACAGCAGAGGCAATTAATG	16-1031L	CTCGGATGTTCCCACTACTCTCTATGCA	16-1031A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1041L	CACCTCTGCTCATCTTTTAC	16-1041R	TAGCTTTCACAAAGCATTTGCTTA	16-1041L	GTCAGTCTCTTTGTGAGGATGTGAAATCA	16-1041A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1051L	ATGAAAGCTGGGTGCTTTGGGTA	16-1051R	ATCAGGGCTCTTCAAGAACT	16-1051L	GGTAGGTGCAAGGTAAATGATTTACCTC	16-1051A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1061L	TCCTCGGGAAGAAAGAACTCA	16-1061R	CTCTCGGAGATGATTTCTCTGTA	16-1061L	CTCTGAGGTGTAAGTCTGCTGTA	16-1061A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1071L	TGCGGCGAGCTGGAATCGG	16-1071R	CGCGCCAGCCGCTGCTCTCTTA	16-1071L	CTCTGAGGTGTAAGTCTGCTGTA	16-1071A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1081L	GCCTCAATGAAGACATCAGCG	16-1081R	GGCAGGATAGTGGCTGGGTAG	16-1081L	CTCTGAGGTGTAAGTCTGCTGTA	16-1081A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1091L	ACTTGTGCTGCTCATGTTA	16-1091R	GCACAAACCGAGGCTGCTCTTA	16-1091L	CTCTGAGGTGTAAGTCTGCTGTA	16-1091A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1101L	GAACCTATTGAACTGTGACCG	16-1101R	CTCTGCTGTAATGTAATCCGTAT	16-1101L	CTCTGAGGTGTAAGTCTGCTGTA	16-1101A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1111L	CTACTGGTATTGAACTGTGACCG	16-1111R	GGGAGCAATATGTAATTTGTA	16-1111L	CTCTGAGGTGTAAGTCTGCTGTA	16-1111A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1121L	TCATATGCTGATGGCATGACCT	16-1121R	GAAAGCAGCAGCAGAGGAA	16-1121L	CTCTGAGGTGTAAGTCTGCTGTA	16-1121A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1131L	TTTACATCTCTACCTGTACAC	16-1131R	TGAATGTATGAGGAGCTCAT	16-1131L	CTCTGAGGTGTAAGTCTGCTGTA	16-1131A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1141L	GTCTCTCATGATCAACATATG	16-1141R	CTCTGATGATGCTGCTGCT	16-1141L	CTCTGAGGTGTAAGTCTGCTGTA	16-1141A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1151L	TGAAAGTCTTCTCTGGGTGCTTA	16-1151R	GAAGCTGATGCTAGATTTGCTGCG	16-1151L	CTCTGAGGTGTAAGTCTGCTGTA	16-1151A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1161L	ACCAGCTGGTGTGTTTCTTAT	16-1161R	TTATCTGTGCGCAGATGGGGACAC	16-1161L	CTCTGAGGTGTAAGTCTGCTGTA	16-1161A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1171L	CAGCTAGACACCAATCTGCTGCTCA	16-1171R	TGTGGATGCTCATATCTATCT	16-1171L	CTCTGAGGTGTAAGTCTGCTGTA	16-1171A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1181L	ATCGCGGTGCTGAGCGGTGA	16-1181R	TCTATTCTCTTCAAAATGTGAC	16-1181L	CTCTGAGGTGTAAGTCTGCTGTA	16-1181A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1191L	GAAATTTTCTTCTCTCTCCCTCT	16-1191R	TGTGAATCTGTGCTCATCTATAGAT	16-1191L	CTCTGAGGTGTAAGTCTGCTGTA	16-1191A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1201L	AAAGGAAATACCAAGTATGCTGCT	16-1201R	CATCAGATGCTCTCACTGCTCTCC	16-1201L	CTCTGAGGTGTAAGTCTGCTGTA	16-1201A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1211L	CAGTAAATCCAGGCGAGATGATG	16-1211R	TGAATATTGGTATGCTGGA	16-1211L	CTCTGAGGTGTAAGTCTGCTGTA	16-1211A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1221L	CGGGGACAAATATTTACCAATC	16-1221R	CTCTTATGCTGCTGCTGCT	16-1221L	CTCTGAGGTGTAAGTCTGCTGTA	16-1221A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1231L	TAGACAAAGGATGATGATCTG	16-1231R	GCTTATGCTGCTGCTGCT	16-1231L	CTCTGAGGTGTAAGTCTGCTGTA	16-1231A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1241L	GCTGGAATTAACATGATGATGAT	16-1241R	ACATTTATGAGCACTGCTGGAAC	16-1241L	CTCTGAGGTGTAAGTCTGCTGTA	16-1241A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1251L	CTCAAGTGCACATGAAACCTTA	16-1251R	TCTAGCAGCGAGAGCAAAATCTGCT	16-1251L	CTCTGAGGTGTAAGTCTGCTGTA	16-1251A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1261L	ATACCATAGCCAGCCCGACAC	16-1261R	GGGGCTCGGAGAGAGAACT	16-1261L	CTCTGAGGTGTAAGTCTGCTGTA	16-1261A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1271L	CTACTGAAATAGAAACTCTGCG	16-1271R	GGACACATGACATCTAGAT	16-1271L	CTCTGAGGTGTAAGTCTGCTGTA	16-1271A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1281L	TGCTGTTGTGCTGCTGCTACTGCT	16-1281R	TCTAAGTCTCTCTGAAAGGCTTA	16-1281L	CTCTGAGGTGTAAGTCTGCTGTA	16-1281A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1291L	TGCTATCATGTAGTACAGATGCAAT	16-1291R	CATCATCAGGCTCTTAAAGCTTGA	16-1291L	CTCTGAGGTGTAAGTCTGCTGTA	16-1291A	GTGAAATAGGATGATGGGGAACAATCCGAG	
16-1301L	CGCGGCCATTTTCACTGCTGCTG	16-1301R	TCCAGAGCGGCTCTTAAAGCTT	16-1301L	CTCTGAGGTGTAAGTCTGCTGTA	16-1301A	GTGAAATAGGATGATGGGGAACAATCCGAG	

Table II

SNP	Left Primer			Labeled Probe			Right Primer		
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')			
16-1311	16-1311L	GCTTGGATTACTAGTGTGTTAT	16-1311R	GGCTGTCTCGAATCCCAAC	16-1311A	TCTGAAGCTTTTGAATAACCTGAGGAGG			
16-1321	16-1321L	TTCCAGATTTTGTGATTTCT	16-1321R	TCCTCGGAGGAGAAATTGAC	16-1321A	GTGGCATTCATTTGATGAGGTTGACAGC			
16-1331	16-1331L	AGACCAAGTGTGTTCTATAGCTAT	16-1331R	ACACTCATGTGTGTTTGAAAT	16-1331A	TAGCTTAGAAGTGGGACGCTTTGAT			
16-1341	16-1341L	TGGCTGGCTGATATATCT	16-1341R	TTGGCTTACAGATCTGGGCG	16-1341A	GAGCAGCTCTG CAGCAGCTCTTTGGAA			
16-1351	16-1351L	ACTGTTCCATGAGAGAT	16-1351R	CTTACACAGGCGGTTGCGTGA	16-1351A	CAGCCTGTTGATGATGCTGATAGATA			
16-1361	16-1361L	GGATTTCCATGTTCATCTCC	16-1361R	AGAGGTGACGAGCTACTTC	16-1361A	CATTCTTGAAGAGCCCGGAGCTCC			
16-1371	16-1371L	CAGCTGTTTAAAGAAATTCG	16-1371R	ACCACGACCTCTCTACGAT	16-1371A	TGGGATTTGCTGCTGATGCTGAGAG			
16-1401	16-1401L	GAGACCACTCTCTGTCACTCA	16-1401R	TTCTGGGCGCCACAGGGGAACC	16-1401A	CAGGTAGGATGTTTGTGATCAAGGATGTC			
Probe on Slide									
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')			
16-1411	16-1411L	GCTGACACTGCTCTTCCCGCA	16-1411R	TGCGGAAACGAGGCGCTGGCATAG	16-1411A	TGGCATAGCTCTGTTTATGACATGAGCTTG			
16-1421	16-1421L	GGGTGGCAGGCTCTCGGTA	16-1421R	GAGCCGCTGCTGCTCTGTGTC	16-1421A	GCCTAGGGGCGCTCTCAGACGCA			
16-1431	16-1431L	CATCAGCTAGGACAGCTCTCTG	16-1431R	CAGAGAGAGCGCTCTGCT	16-1431A	GGCCATCATCTCTAGAGAGCGGAGAA			
16-1451	16-1451L	AGACCACTGCTGCTGACAGACTA	16-1451R	GGGTGACAGCTCTGGGTG	16-1451A	GGTGTGGGATTCAGTCTCCATCTCTTA			
16-1461	16-1461L	GGTGGCGCCAGGTTTAGAG	16-1461R	AGAGGTGGGAGAGGCGGCTTA	16-1461A	CTGGCTGGTTTGTAGTCCGGTAACTTTTC			
16-1471	16-1471L	GAATTTGGTTTGAATCTGGGTA	16-1471R	ATTCATGATCCCAACAACT	16-1471A	TGAGATCACTCCAGTAAAGGATGTTGTG			
16-1481	16-1481L	TCAGAGCAAGCTGAGGATA	16-1481R	CACTTATGATAGACTTCATCTAA	16-1481A	GTATGATACCTCTGATATGCTCTGG			
16-1501	16-1501L	AGCCAGACTCAACACTCTTA	16-1501R	GAACAGGCGGACAGGAACTG	16-1501A	CTCTGATTTACCTAAATATCAGTGAAG			
16-1511	16-1511L	TTCCCGACTCTCTGTATC	16-1511R	CAGCCAGACTCGATCCCTCTATC	16-1511A	GAAGTACCTCTAAAGCAAGGCTGAGAT			
16-1521	16-1521L	TGGGTACCTCTGGGAGAAATG	16-1521R	CAGCCAGCTGAGAACTGTC	16-1521A	CAGACCAGCGGTGAAGCAAGGGGAA			
16-1531	16-1531L	TCGCGACTCTAGGCTTACCGG	16-1531R	CAGCCAGCTGAGAACTGTC	16-1531A	CGGCATTTCTAGCAAGATTTGGAAGCC			
16-1551	16-1551L	TTCCAACTCTAGCTCTGCGG	16-1551R	AGAGAGCTTGAAGGCTGACTG	16-1551A	TGCGATCTGATGCAAGATGCTGACAGC			
16-1561	16-1561L	CAGAGCTCTAGGCTGCTGAT	16-1561R	CTCTGAGTCTGAGAACTGTC	16-1561A	GGTCAAGGCGCACTCGGCTGGCT			
16-1571	16-1571L	AGAGGTTCAAGGCTGCTGATG	16-1571R	CTCTGAGTCTGAGAACTGTC	16-1571A	GTTTAAAGAGGACATGATCTTGAGGTGGA			
16-1581	16-1581L	CTTAACTGCTCTCTTGGGTCTCA	16-1581R	AGCCATGCTGAGCAAGCGG	16-1581A	CTGCTATCTGCTGATGCTGTC			
16-1591	16-1591L	TGGCTCTAGAAATACTTCA	16-1591R	CATTCTGCTGATGCACTGTC	16-1591A	CTGCTATCTGCTGATGCTGTC			
16-1601	16-1601L	CTGTCTATTGTTGTGCTAA	16-1601R	CTCTGGCAACCAACAGTA	16-1601A	TCCTATCCCAAGCCCCCTGACTTCCA			
16-1611	16-1611L	AGCCTCTAGGGGAGGCAAC	16-1611R	GGGCCATCTCCCGCACTAATAG	16-1611A	TGGAAGTCTGAGGGCGCTGGGATGGA			
16-1621	16-1621L	CAGAGAGCGCGCGAGCTGGC	16-1621R	AGCAAGAGTGTCCAGCTGGC	16-1621A	CTGGGAGAGAGGCTGGGCTCAAGG			
16-1631	16-1631L	TGCTCTCTCTCAATAGAGAGTTAT	16-1631R	CCCTCTCTGCTCTAGTGGTGCTTA	16-1631A	GCACATGMAATCATGAGGCTGCACAGGA			
16-1651	16-1651L	TGATATCTTCAACAGCTTTCC	16-1651R	TGATGACTCTGATTAACCGTA	16-1651A	GGCAGTGTCTATGGAATTTCTCTCCAC			
16-1661	16-1661L	CCAGCAGGATTTAGAGCCAGGGCA	16-1661R	AAGGAGCGGTGTCCAGCGGT	16-1661A	CGCAGTGTCTATGGAATTTCTCTCCAC			
16-1671	16-1671L	GCCTCCTGGGCGCTCTGCTTA	16-1671R	TTGTTCACACCCATGTCAATA	16-1671A	CTGTCTCTCTCAAGAGGCTGACCCACC			
16-1681	16-1681L	CTCCACATGCGCTCTTGATTA	16-1681R	CTGATGTCCCATCACCAGCGGGCA	16-1681A	GGCATGGGTCACTGGGAAGGCCACAG			
16-1691	16-1691L	GTGTGAGCTGGTCCAGGCCAACG	16-1691R	ATGTGTTTAAAGAGGTTTCCCTCTA	16-1691A	CTGAGGACAGTCTCCAGAGTGTGGG			
16-1701	16-1701L	ATGGTTTATGTCAACCCGGA	16-1701R	AGATCGGACCGTAGAATCTAAAT	16-1701A	TTTGAGTTGATGTTAACTCTCTCTGCTG			
16-1741	16-1741L	GGGGCTCTTTAGAGAAAGTTGAC	16-1741R	ATGAGTCTGCTGGGAGAGG	16-1741A	CTTGAGGCTGTTCATGCTCTCTGCTGA			
16-1751	16-1751L	TTGGCGCTCAGCAGAGGGCG	16-1751R	TTAGAGAGCTGCTCTCCGCTG	16-1751A	GAGCGTCTCTAGAGAGAGGCTCCAGC			
16-1761	16-1761L	CCCTCTCAGATGAGGTGGGT	16-1761R	TTATGAGGCTCTGCTGCTGCTG	16-1761A	GGGCTCTCTAGAGAGGCTCTGCTGCTG			
16-1771	16-1771L	GTTTATGATGATGAGTCTTTGAC	16-1771R	TTATGAGGCTCTGCTGCTGCTG	16-1771A	CAAGAAGCTCTCTGCTGCTGCTGCTG			
16-1781	16-1781L	CAATCTAGAAAGCGGGCAAT	16-1781R	CTCAGCTGCTCTTTGCTCT	16-1781A	AATGGGTAACTGATCTACCGCTGACTAGGC			
16-1791	16-1791L	TGAACATAAGTGTGAGGCAAC	16-1791R	AGGAAGTATCTGAGGAGTGTGTTA	16-1791A	GGGCTCTGAGAGGCTCTAACTGATGCTATC			
16-1801	16-1801L	CCCATAGACATGAGAGGCAAT	16-1801R	AGGAGTGTGATGAGGAGGCTG	16-1801A	CAGCTTGGCAGGCTGAGGCTGCTCT			
16-1811	16-1811L	AAGTAAAGATGAGCAGAACG	16-1811R	AGAGTGTGATGAGGAGGCTG	16-1811A	TCACGAGGAGCAGGAGGCGGCTCT			
16-1821	16-1821L	TTTCTTATGGGATTTCTACAG	16-1821R	ATGCTCTGCTGGGAGAGG	16-1821A	ACACGACAGACGCCCCACCCGAG			
16-1831	16-1831L	TAGACTCTATGATGCTGCTG	16-1831R	TTTCTCTATTTGGGCAACCGG	16-1831A	ATGCTCTATGTCAGATGGAAGTGAAGGA			
16-2003L	16-2003L	AGCATTTTGGGAGCCGCAAGC	16-2003R	CACAGTTTCAACAACAATTTATC	20-0031A	TTCTATAGGCTGAGATTAATGAGCAGCG			
16-2005L	16-2005L	GATTTGCTCTGACAGCGGCTAT	16-2005R	TCAGAGAAATGCTGCTTTATC	20-0051A	CACATGACACTTTATGTCGGCTCAGTT			
16-2007L	16-2007L	GAATCATGCTATCTGCTGTGAG	16-2007R	TGACACTAATGGAATGTAACTTC	20-0071A	AGCCAGATTTCTCTCTTCAACTCCCA			
16-2008L	16-2008L	CAGGTGATGGAAGGCTGTCTCTAT	16-2008R	TGTCTCTAAATATCCCAACAC	20-0081A	ACCTCTTTGATGAGGACGATTTCTCCCA			
16-2010L	16-2010L	ACAAGATGGAATTTACATCTGTA	16-2010R	AGGCTGAGAGCAAGAAACCGT	20-0101A	GTTCATCTCAACAGTTATTTGATGAGCA			
16-2011L	16-2011L	GCAAOTGGGCAATGATCTCTG	16-2011R	TAAAGCAACTCTTATTTGAGTTC	20-0111A	ATTCCTGAGAGACTTATGATGCTATCT			
16-2012L	16-2012L	TGTTTCTCATGAAATCTTTTA	16-2012R	GGTCTGGACACAAACCTTGC	20-0121A	TTTCTCTGTGATGATTAATCAGCAGGAG			
16-2013L	16-2013L	CTTGCGGAAGGGGCACTAA	16-2013R	TATCCAGATCTTGGTCACTCG	20-0131A	TTTCAATTAATCAAGACTTGGGCACTGGT			

Table 11

SNP	Name	Sequence (from 5' to 3')	Left Primer	Name	Sequence (from 5' to 3')	Right Primer	Name	Sequence (from 5' to 3')	Right Primer
20-0141	20-0141	TGCACACAGCTATATCTTCT	AGTACTCGTGGCTGGGACACG	20-0141	AGTACTCGTGGCTGGGACACG	20-0141	20-0141	CGCAGGGACACTCACTCTCAGGAAC	20-0141
20-0151	20-0151	TCCACTGCTGCTCTCTATGACAT	AAGATCAGAAAGCTCTCAT	20-0151	AAGATCAGAAAGCTCTCAT	20-0151	20-0151	GGCTATGTTTATTTCTGCTGCTATCAT	20-0151
20-0171	20-0171	CCCTACTGCTGCTCTCTCTCTCT	TGTCACCTGGGACACATTTAT	20-0171	TGTCACCTGGGACACATTTAT	20-0171	20-0171	CACTCTGCGCCCTGCTCTCTCTCT	20-0171
20-0191	20-0191	AAATAAGTAAGCTCTCTCTCTCT	TATCAGAGGCTGAAATGAGCTAA	20-0191	TATCAGAGGCTGAAATGAGCTAA	20-0191	20-0191	CTACATATAATGCTATTAATTAAGAGGTAT	20-0191
20-0211	20-0211	GAATGAACAGCTAGAGATGTTA	AGGCACTCTCTCTCTCTCTCTCT	20-0211	AGGCACTCTCTCTCTCTCTCTCT	20-0211	20-0211	TCTTGAAGCTTGTAGTACGATTTATGCTCT	20-0211
20-0231	20-0231	GAATGAACAGCTAGAGATGTTA	TGTAAGTGTGTCTCTCTCTCT	20-0231	TGTAAGTGTGTCTCTCTCTCTCT	20-0231	20-0231	GTGACCTTTTAAAGAAAGCACTATGACG	20-0231
20-0251	20-0251	GGGGTTCAGAAATGCTCAATAACG	CACCTGCTGTAGCTCTCTCTCT	20-0251	CACCTGCTGTAGCTCTCTCTCTCT	20-0251	20-0251	GAAGTACTTGGCAGGTTTCTGCTGGGACCA	20-0251
20-0261	20-0261	CAGAGATTGGAACCAACAGATATG	ATCCCTGCTAGCTGAGCTCTCTA	20-0261	ATCCCTGCTAGCTGAGCTCTCTA	20-0261	20-0261	ATGATCTTCCATTTGCTCTCTGATTTCAA	20-0261
20-0281	20-0281	TAAAGCCATCTCTGTTGCTCTG	AGTCAGTTGGAGATTTCTCTAT	20-0281	AGTCAGTTGGAGATTTCTCTAT	20-0281	20-0281	CTCTGTTTAAAGCCACAGAGAGAGGACGG	20-0281
20-0291	20-0291	AGGAGAGAGGATATGGGAAAAA	TGAACCCAGCAATTTGGCTCTCA	20-0291	TGAACCCAGCAATTTGGCTCTCA	20-0291	20-0291	AGGTCATCTGCTGGGACCAAGGCAAAAAGT	20-0291
20-0301	20-0301	TTTGTATCCAGATGAAAAA	TATACCTGCTCTCTCTCTCTCTCT	20-0301	TATACCTGCTCTCTCTCTCTCTCT	20-0301	20-0301	CAITCAAAGTGAAGATTAATTAACATAGCC	20-0301
20-0311	20-0311	AGAGGGTTTAAAGAGGTTGCAAT	TGTCATACAGAGACCTCAAT	20-0311	TGTCATACAGAGACCTCAAT	20-0311	20-0311	GAGGAAGTAAATGAGAAATATTAATACAAAT	20-0311
20-0321	20-0321	CATTACAGTTTCTGCAATCT	TTCCTTCAACCACTCTCTCTCT	20-0321	TTCCTTCAACCACTCTCTCTCTCT	20-0321	20-0321	TTACTTATCTAAGTCTTCTTACGACAAGAG	20-0321
20-0331	20-0331	CATTACAGTTTCTGCAATCT	TATCCACCACTCTCTCTCTCTCT	20-0331	TATCCACCACTCTCTCTCTCTCT	20-0331	20-0331	CTAGCTCTTATGCTCTTATCTCTATATG	20-0331
20-0341	20-0341	AGGCTTGTCTTAAAGTCTAGAT	ATCCAGAGTGGTGTAGAGGATAG	20-0341	ATCCAGAGTGGTGTAGAGGATAG	20-0341	20-0341	CTCCCTCTTATGCTCTTATCTCTATATG	20-0341
20-0351	20-0351	CGATATCAAAATGCTCTTGTGA	AAGGAAGTCTCTCTCTCTCTCT	20-0351	AAGGAAGTCTCTCTCTCTCTCTCT	20-0351	20-0351	CTAGCTCTTATGCTCTTATCTCTATATG	20-0351
20-0361	20-0361	ACAAAGCAGAGTGCAGAGGATG	ATTTGGAACAAGGGTCTCTCT	20-0361	ATTTGGAACAAGGGTCTCTCTCT	20-0361	20-0361	GTATGCGAGGAGGAGGCTCTACAGGACTG	20-0361
20-0371	20-0371	TGGCCCTGATCCCAACAAAC	TGTCATATCAAGTCTCTCTCTCT	20-0371	TGTCATATCAAGTCTCTCTCTCTCT	20-0371	20-0371	CTAGATATCTCAACATCTCTCTCTCTCT	20-0371
20-0381	20-0381	GAGACTGTACAGCACTGTAG	CACCTTACCTAGTCTCTCTCTCT	20-0381	CACCTTACCTAGTCTCTCTCTCTCT	20-0381	20-0381	CGATAGTCTCTATTTCTCTCTCTCTCTCT	20-0381
20-0391	20-0391	GCTGGAATTTCTCTCTCTCTCT	TCCCAAGGCTCTCTCTCTCTCTCT	20-0391	TCCCAAGGCTCTCTCTCTCTCTCT	20-0391	20-0391	TGCTCTGCTGCTGCTGCTGCTGCTGCT	20-0391
20-0401	20-0401	GAATCTAACTCTCTCTCTCTCT	AGGAGTCTCTCTCTCTCTCTCT	20-0401	AGGAGTCTCTCTCTCTCTCTCTCT	20-0401	20-0401	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0401
20-0411	20-0411	CTTAAGCAGATATGCTCTCAAT	TGAGCAGTCTCTCTCTCTCTCT	20-0411	TGAGCAGTCTCTCTCTCTCTCTCT	20-0411	20-0411	GTCTCTGCTTATACAGGCTCTGTAAGTGT	20-0411
20-0421	20-0421	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0421	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0421	20-0421	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0421
20-0431	20-0431	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0431	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0431	20-0431	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0431
20-0441	20-0441	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0441	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0441	20-0441	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0441
20-0451	20-0451	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0451	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0451	20-0451	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0451
20-0461	20-0461	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0461	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0461	20-0461	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0461
20-0471	20-0471	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0471	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0471	20-0471	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0471
20-0481	20-0481	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0481	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0481	20-0481	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0481
20-0491	20-0491	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0491	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0491	20-0491	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0491
20-0501	20-0501	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0501	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0501	20-0501	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0501
20-0511	20-0511	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0511	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0511	20-0511	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0511
20-0521	20-0521	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0521	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0521	20-0521	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0521
20-0531	20-0531	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0531	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0531	20-0531	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0531
20-0541	20-0541	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0541	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0541	20-0541	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0541
20-0551	20-0551	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0551	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0551	20-0551	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0551
20-0561	20-0561	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0561	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0561	20-0561	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0561
20-0571	20-0571	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0571	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0571	20-0571	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0571
20-0581	20-0581	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0581	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0581	20-0581	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0581
20-0591	20-0591	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0591	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0591	20-0591	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0591
20-0601	20-0601	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0601	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0601	20-0601	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0601
20-0611	20-0611	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0611	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0611	20-0611	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0611
20-0621	20-0621	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0621	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0621	20-0621	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0621
20-0631	20-0631	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0631	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0631	20-0631	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0631
20-0641	20-0641	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0641	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0641	20-0641	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0641
20-0651	20-0651	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0651	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0651	20-0651	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0651
20-0661	20-0661	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0661	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0661	20-0661	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0661
20-0671	20-0671	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0671	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0671	20-0671	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0671
20-0681	20-0681	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0681	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0681	20-0681	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0681
20-0691	20-0691	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0691	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0691	20-0691	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0691
20-0701	20-0701	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0701	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0701	20-0701	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0701
20-0711	20-0711	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0711	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0711	20-0711	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0711
20-0721	20-0721	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0721	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0721	20-0721	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0721
20-0731	20-0731	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0731	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0731	20-0731	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0731
20-0741	20-0741	GTAGTGTGGAGTCTCTCTCTCT	TAATCTGAGGCTCTCTCTCTCTCT	20-0741	TAATCTGAGGCTCTCTCTCTCTCTCT	20-0741	20-0741	TTCAAGGAGGAGGAGGAGGAGGAGGAG	20-0741

SNP	Name	Sequence (from 5' to 3')	Left Primer	Name	Sequence (from 5' to 3')	Right Primer	Name	Sequence (from 5' to 3')	Probe on Slide	
20-0751	20-0751	GAGATACAGATTATATATAT	20-0751	20-0751	GTCACCAAGAGGCTCACACAT	20-0751	20-0751	TGTGACCTCTGTATGTCTCTCAAGAGATGA	20-0751	TCATCTCTTGTGAGACATACAAAGGTGCACA
20-0761	20-0761	GTTCCTACGACAGCAATCCG	20-0761	20-0761	AGCCCATGCGTGTCAACATAA	20-0761	20-0761	ATGATCAAACTACCTCTCTATACAGAAC	20-0761	TGTTCTGCTAGAGGATGAGTGTGATCAT
20-0771	20-0771	TGGAGGAAATGTTTAAAGCAT	20-0771	20-0771	AGAAATTTTCCACCATATGCTG	20-0771	20-0771	CACCACCAAGGAAAGGCTATATATAGT	20-0771	ATCTAATAATAGCTCTCTTTTGTGTGTG
20-0781	20-0781	GGACCTTGGGTGCAGATCAAAAC	20-0781	20-0781	AGCACTCTCAGCAGTGAAGATAG	20-0781	20-0781	ATGTCACGACAGGTGAGCCCAACATC	20-0781	GAGTGTGGGCTTACCTGCTGTGACAT
20-0791	20-0791	GGCCATGGCATGTGTTTCAAAAGT	20-0791	20-0791	ATGCTATGTTTGAAGAAAAA	20-0791	20-0791	CTGTAGCACTGCTATGGCTCTTCTG	20-0791	CAGAAAGCCCAATGCTGCTGAC
20-0801	20-0801	GGATCTAGAACACCCCTAGT	20-0801	20-0801	TCATCTACTCTCTTCAAGGGA	20-0801	20-0801	CTGTGTCACCAAGAGTGTGATGCT	20-0801	ACCAAGTCCATCTGCGGTGGGCTAGG
20-0811	20-0811	TAACTCTAACTAGATCTCTCTA	20-0811	20-0811	ATAGTGGGAGGTCTGGGTA	20-0811	20-0811	TATCCAGGGCTCACTGGGGTCTGTTT	20-0811	AAACAGAACCCAAAGTGGCTGAGATA
20-0821	20-0821	CATTGGTATGAGTGGTCTGTA	20-0821	20-0821	ACCTTCTCTCTAGGGGACAG	20-0821	20-0821	AAGCCTCTTCTCTCTATATGTTGCTT	20-0821	CAAGCAATAAGAGAGGATAGGCTGCT
20-0831	20-0831	TCCAGAGCTGTAAATAGCTG	20-0831	20-0831	TTCAGATGTTCTTCCAGTA	20-0831	20-0831	CCAGTACTTGTATCTCTATGTTCTGCA	20-0831	TCGAAACCATCAGATACAAAGTACGGA
20-0841	20-0841	CATCTTCAGTGACTGATGATAGT	20-0841	20-0841	TTTCCAGAACATTAATGCT	20-0841	20-0841	TCCATGCTGATCTTCCCAAGACTGA	20-0841	TCAGTCTGGGACAGACTGACCAAGTGG
20-0851	20-0851	TGCTCTATGTTCCGGATAAGTA	20-0851	20-0851	TGCGCAAGCGTCTCTCTTA	20-0851	20-0851	ACTCAATAGCCACAGTGAAGTGCCTATG	20-0851	CATGAGGCACTTCTGCTGTGCTTATGAT
20-0861	20-0861	TGCGCTGAGATGTGAACCT	20-0861	20-0861	TGCGCTCAAGCTATCTTCCACC	20-0861	20-0861	GGTGTGAGCCACACACCCCGGCC	20-0861	GGCGCGGTGTGCTGCTGCTCACACC
20-0871	20-0871	TCTTGGCTTGGCTGAGATCTTAA	20-0871	20-0871	AGGAGTCCATCTTCCAGACTAA	20-0871	20-0871	GTGGGTGAGGAGCCACTATGCTTCTC	20-0871	GAGAAAAGCATGAGTGGCTCTCTCACCCAC
20-0881	20-0881	GGTACGAGTGTGATGTTGAGGCT	20-0881	20-0881	GGTTCCTCCAGCAATGGGAACT	20-0881	20-0881	TATAGTGTGTTTCTACTGCTGTAAGACA	20-0881	TGTCTTATCAGCATGATGTAACACAGACTAATA
20-0891	20-0891	CCACTGTTCCCATATTTCTG	20-0891	20-0891	ATTATGCGCAAAATGGTCTGAC	20-0891	20-0891	CATTCTGTGTCTACTCAATACAGTAT	20-0891	ATAGTGTATGAGGTAGACACAGAAATG
20-0901	20-0901	GAGATCAGACCTAACCACTCTA	20-0901	20-0901	TGTTTCACTCAAACTAACT	20-0901	20-0901	AATAAATCTCTCTAAGTTAGTCTG	20-0901	GCAGAACTAACCTTAAGAAAGGATTTAGTT
20-0911	20-0911	GTCTGTACAGTTTCCAGAGGTTA	20-0911	20-0911	GGCCCTTTTATAAAGTAACTAA	20-0911	20-0911	CATCACTCTGATAGCTAAATGGAAGTATGA	20-0911	TCATACCTTCTTCAATGCTATCAGAGTATG
20-0921	20-0921	TCCACAAAATGGGAAGCT	20-0921	20-0921	ACAATCTTCAAGAAATCAAGAT	20-0921	20-0921	AGGGGACACAACTCAACCCATGECAT	20-0921	ATGCCATGGTGTGAGTGTGCTCCCT
20-0931	20-0931	AGTCTGACGTGAGCAGGCTTA	20-0931	20-0931	GGGTAGTTTGGCTGAGGAGTGC	20-0931	20-0931	CTTTGTCACCTCAACCCCAATATCAAC	20-0931	GGTGTATATGCTGGGTGTGAGTGCACAGC
20-0941	20-0941	CGAACTAACTTCCATGGA	20-0941	20-0941	AGGTCTAGACTATCAAGCACT	20-0941	20-0941	ATCACACATAGATTAAGAAAGTGTG	20-0941	ACCACTCTTCTTCTAATCTATGCTGTAT
20-0951	20-0951	ATCTCATCTGAGCATATTAATA	20-0951	20-0951	GGCTCCGCTTTTGAAGCTAT	20-0951	20-0951	TTATGATGATGTTTCCAAACAGTGGCA	20-0951	TGCCCTGTTTGGGAAACATCATCTAATA
20-0961	20-0961	TGATGAGGATACATATTTCAAC	20-0961	20-0961	TGAGTTTTCAGGAGCAAAAC	20-0961	20-0961	CACCACTACGCGGTGAGTGAAGTAA	20-0961	CATTCAGCTACTAGCCCCGTAGCTGTG
20-0971	20-0971	CCAGGCGCTGGACCCGTTA	20-0971	20-0971	GAGGCTTAAATGGGAGCCCT	20-0971	20-0971	ACTCACTGCTCCACCCCTCAAGCTTC	20-0971	GAAGCTGATGGGCTGAGAGCACTGAT
20-0981	20-0981	TGATGAGGATGAGTGTGAGT	20-0981	20-0981	ATATGCAATTTGCAACCTT	20-0981	20-0981	OACCTCTGATCTTCTTGTGCTCTAA	20-0981	TAGGGGACCAAGAAAGATCAGAGGCTC
20-0991	20-0991	CTGTGAGCACTGGATCTAT	20-0991	20-0991	TGAGGAGGAGTGAAGATGAC	20-0991	20-0991	ATCTTCTGAGCTCAAGGATTCAGATAA	20-0991	TTACCTGGAACTCCCTGGAGCTCAGAGAT
20-1001	20-1001	CCCTTCTGAGAGGCTATGTAACA	20-1001	20-1001	GGGTAAGGCAAGTAAAGTGTAT	20-1001	20-1001	AAGGGGCTTGAACATGGGATGCTA	20-1001	TAGCATCCCATGTGTCAAGGCCCTT
20-1011	20-1011	CCCTTCTGAGAGGCTATGTAACA	20-1011	20-1011	GGGTAAGGCAAGTAAAGTGTAT	20-1011	20-1011	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1011	CCAGGAGTGTGCTCCCAAGCTCTGAAA
20-1021	20-1021	CCCTTCTGAGAGGCTATGTAACA	20-1021	20-1021	GGGTAAGGCAAGTAAAGTGTAT	20-1021	20-1021	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1021	TGGCTCTCGGCTCTTCTGATGAG
20-1031	20-1031	CCCTTCTGAGAGGCTATGTAACA	20-1031	20-1031	GGGTAAGGCAAGTAAAGTGTAT	20-1031	20-1031	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1031	AACATGACATTAAGCCCTTCTTAACACTTA
20-1041	20-1041	CCCTTCTGAGAGGCTATGTAACA	20-1041	20-1041	GGGTAAGGCAAGTAAAGTGTAT	20-1041	20-1041	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1041	GTATGAGTGCATGGGTGAGGCTCTCTC
20-1051	20-1051	CCCTTCTGAGAGGCTATGTAACA	20-1051	20-1051	GGGTAAGGCAAGTAAAGTGTAT	20-1051	20-1051	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1051	TCATGCTGCTGATGCTGCTCTGATGAT
20-1061	20-1061	CCCTTCTGAGAGGCTATGTAACA	20-1061	20-1061	GGGTAAGGCAAGTAAAGTGTAT	20-1061	20-1061	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1061	ATTACTGGCAGGATTCATTAATACCACTG
20-1071	20-1071	CCCTTCTGAGAGGCTATGTAACA	20-1071	20-1071	GGGTAAGGCAAGTAAAGTGTAT	20-1071	20-1071	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1071	GGTGTGCAAGAGTCTGACCTTGGCT
20-1081	20-1081	CCCTTCTGAGAGGCTATGTAACA	20-1081	20-1081	GGGTAAGGCAAGTAAAGTGTAT	20-1081	20-1081	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1081	GGTGTGCAAGAGTCTGACCTTGGCT
20-1091	20-1091	CCCTTCTGAGAGGCTATGTAACA	20-1091	20-1091	GGGTAAGGCAAGTAAAGTGTAT	20-1091	20-1091	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1091	GGTGTGCAAGAGTCTGACCTTGGCT
20-1101	20-1101	CCCTTCTGAGAGGCTATGTAACA	20-1101	20-1101	GGGTAAGGCAAGTAAAGTGTAT	20-1101	20-1101	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1101	GGTGTGCAAGAGTCTGACCTTGGCT
20-1111	20-1111	CCCTTCTGAGAGGCTATGTAACA	20-1111	20-1111	GGGTAAGGCAAGTAAAGTGTAT	20-1111	20-1111	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1111	GGTGTGCAAGAGTCTGACCTTGGCT
20-1121	20-1121	CCCTTCTGAGAGGCTATGTAACA	20-1121	20-1121	GGGTAAGGCAAGTAAAGTGTAT	20-1121	20-1121	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1121	GGTGTGCAAGAGTCTGACCTTGGCT
20-1131	20-1131	CCCTTCTGAGAGGCTATGTAACA	20-1131	20-1131	GGGTAAGGCAAGTAAAGTGTAT	20-1131	20-1131	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1131	GGTGTGCAAGAGTCTGACCTTGGCT
20-1141	20-1141	CCCTTCTGAGAGGCTATGTAACA	20-1141	20-1141	GGGTAAGGCAAGTAAAGTGTAT	20-1141	20-1141	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1141	GGTGTGCAAGAGTCTGACCTTGGCT
20-1151	20-1151	CCCTTCTGAGAGGCTATGTAACA	20-1151	20-1151	GGGTAAGGCAAGTAAAGTGTAT	20-1151	20-1151	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1151	GGTGTGCAAGAGTCTGACCTTGGCT
20-1161	20-1161	CCCTTCTGAGAGGCTATGTAACA	20-1161	20-1161	GGGTAAGGCAAGTAAAGTGTAT	20-1161	20-1161	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1161	GGTGTGCAAGAGTCTGACCTTGGCT
20-1171	20-1171	CCCTTCTGAGAGGCTATGTAACA	20-1171	20-1171	GGGTAAGGCAAGTAAAGTGTAT	20-1171	20-1171	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1171	GGTGTGCAAGAGTCTGACCTTGGCT
20-1181	20-1181	CCCTTCTGAGAGGCTATGTAACA	20-1181	20-1181	GGGTAAGGCAAGTAAAGTGTAT	20-1181	20-1181	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1181	GGTGTGCAAGAGTCTGACCTTGGCT
20-1191	20-1191	CCCTTCTGAGAGGCTATGTAACA	20-1191	20-1191	GGGTAAGGCAAGTAAAGTGTAT	20-1191	20-1191	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1191	GGTGTGCAAGAGTCTGACCTTGGCT
20-1201	20-1201	CCCTTCTGAGAGGCTATGTAACA	20-1201	20-1201	GGGTAAGGCAAGTAAAGTGTAT	20-1201	20-1201	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1201	GGTGTGCAAGAGTCTGACCTTGGCT
20-1211	20-1211	CCCTTCTGAGAGGCTATGTAACA	20-1211	20-1211	GGGTAAGGCAAGTAAAGTGTAT	20-1211	20-1211	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1211	GGTGTGCAAGAGTCTGACCTTGGCT
20-1221	20-1221	CCCTTCTGAGAGGCTATGTAACA	20-1221	20-1221	GGGTAAGGCAAGTAAAGTGTAT	20-1221	20-1221	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1221	GGTGTGCAAGAGTCTGACCTTGGCT
20-1231	20-1231	CCCTTCTGAGAGGCTATGTAACA	20-1231	20-1231	GGGTAAGGCAAGTAAAGTGTAT	20-1231	20-1231	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1231	GGTGTGCAAGAGTCTGACCTTGGCT
20-1241	20-1241	CCCTTCTGAGAGGCTATGTAACA	20-1241	20-1241	GGGTAAGGCAAGTAAAGTGTAT	20-1241	20-1241	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1241	GGTGTGCAAGAGTCTGACCTTGGCT
20-1251	20-1251	CCCTTCTGAGAGGCTATGTAACA	20-1251	20-1251	GGGTAAGGCAAGTAAAGTGTAT	20-1251	20-1251	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1251	GGTGTGCAAGAGTCTGACCTTGGCT
20-1261	20-1261	CCCTTCTGAGAGGCTATGTAACA	20-1261	20-1261	GGGTAAGGCAAGTAAAGTGTAT	20-1261	20-1261	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1261	GGTGTGCAAGAGTCTGACCTTGGCT
20-1271	20-1271	CCCTTCTGAGAGGCTATGTAACA	20-1271	20-1271	GGGTAAGGCAAGTAAAGTGTAT	20-1271	20-1271	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1271	GGTGTGCAAGAGTCTGACCTTGGCT
20-1281	20-1281	CCCTTCTGAGAGGCTATGTAACA	20-1281	20-1281	GGGTAAGGCAAGTAAAGTGTAT	20-1281	20-1281	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1281	GGTGTGCAAGAGTCTGACCTTGGCT
20-1291	20-1291	CCCTTCTGAGAGGCTATGTAACA	20-1291	20-1291	GGGTAAGGCAAGTAAAGTGTAT	20-1291	20-1291	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1291	GGTGTGCAAGAGTCTGACCTTGGCT
20-1301	20-1301	CCCTTCTGAGAGGCTATGTAACA	20-1301	20-1301	GGGTAAGGCAAGTAAAGTGTAT	20-1301	20-1301	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1301	GGTGTGCAAGAGTCTGACCTTGGCT
20-1311	20-1311	CCCTTCTGAGAGGCTATGTAACA	20-1311	20-1311	GGGTAAGGCAAGTAAAGTGTAT	20-1311	20-1311	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1311	GGTGTGCAAGAGTCTGACCTTGGCT
20-1321	20-1321	CCCTTCTGAGAGGCTATGTAACA	20-1321	20-1321	GGGTAAGGCAAGTAAAGTGTAT	20-1321	20-1321	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1321	GGTGTGCAAGAGTCTGACCTTGGCT
20-1331	20-1331	CCCTTCTGAGAGGCTATGTAACA	20-1331	20-1331	GGGTAAGGCAAGTAAAGTGTAT	20-1331	20-1331	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1331	GGTGTGCAAGAGTCTGACCTTGGCT
20-1341	20-1341	CCCTTCTGAGAGGCTATGTAACA	20-1341	20-1341	GGGTAAGGCAAGTAAAGTGTAT	20-1341	20-1341	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1341	GGTGTGCAAGAGTCTGACCTTGGCT
20-1351	20-1351	CCCTTCTGAGAGGCTATGTAACA	20-1351	20-1351	GGGTAAGGCAAGTAAAGTGTAT	20-1351	20-1351	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1351	GGTGTGCAAGAGTCTGACCTTGGCT
20-1361	20-1361	CCCTTCTGAGAGGCTATGTAACA	20-1361	20-1361	GGGTAAGGCAAGTAAAGTGTAT	20-1361	20-1361	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1361	GGTGTGCAAGAGTCTGACCTTGGCT
20-1371	20-1371	CCCTTCTGAGAGGCTATGTAACA	20-1371	20-1371	GGGTAAGGCAAGTAAAGTGTAT	20-1371	20-1371	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1371	GGTGTGCAAGAGTCTGACCTTGGCT
20-1381	20-1381	CCCTTCTGAGAGGCTATGTAACA	20-1381	20-1381	GGGTAAGGCAAGTAAAGTGTAT	20-1381	20-1381	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1381	GGTGTGCAAGAGTCTGACCTTGGCT
20-1391	20-1391	CCCTTCTGAGAGGCTATGTAACA	20-1391	20-1391	GGGTAAGGCAAGTAAAGTGTAT	20-1391	20-1391	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1391	GGTGTGCAAGAGTCTGACCTTGGCT
20-1401	20-1401	CCCTTCTGAGAGGCTATGTAACA	20-1401	20-1401	GGGTAAGGCAAGTAAAGTGTAT	20-1401	20-1401	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1401	GGTGTGCAAGAGTCTGACCTTGGCT
20-1411	20-1411	CCCTTCTGAGAGGCTATGTAACA	20-1411	20-1411	GGGTAAGGCAAGTAAAGTGTAT	20-1411	20-1411	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1411	GGTGTGCAAGAGTCTGACCTTGGCT
20-1421	20-1421	CCCTTCTGAGAGGCTATGTAACA	20-1421	20-1421	GGGTAAGGCAAGTAAAGTGTAT	20-1421	20-1421	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1421	GGTGTGCAAGAGTCTGACCTTGGCT
20-1431	20-1431	CCCTTCTGAGAGGCTATGTAACA	20-1431	20-1431	GGGTAAGGCAAGTAAAGTGTAT	20-1431	20-1431	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1431	GGTGTGCAAGAGTCTGACCTTGGCT
20-1441	20-1441	CCCTTCTGAGAGGCTATGTAACA	20-1441	20-1441	GGGTAAGGCAAGTAAAGTGTAT	20-1441	20-1441	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1441	GGTGTGCAAGAGTCTGACCTTGGCT
20-1451	20-1451	CCCTTCTGAGAGGCTATGTAACA	20-1451	20-1451	GGGTAAGGCAAGTAAAGTGTAT	20-1451	20-1451	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1451	GGTGTGCAAGAGTCTGACCTTGGCT
20-1461	20-1461	CCCTTCTGAGAGGCTATGTAACA	20-1461	20-1461	GGGTAAGGCAAGTAAAGTGTAT	20-1461	20-1461	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1461	GGTGTGCAAGAGTCTGACCTTGGCT
20-1471	20-1471	CCCTTCTGAGAGGCTATGTAACA	20-1471	20-1471	GGGTAAGGCAAGTAAAGTGTAT	20-1471	20-1471	TTTCAAGGCTTGGGAGCAGCTCTGG	20-1471	GGTGTGCAAGAGTCTGACCTTGGCT
20-1481	20-1481	CCCTTCTGAGAGGCTATGTAACA	20-1481	20-1481	GGGTAAGGCAAGTAAAGTGTAT	20-1481	20-			

SNP	Left Primer			Labeled Probi			Probe on Slide		
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	
22-0081	22-0081	CCCCAGGCTGACTCAAGATGTC	22-0081	GAGGCTTCTAGACACTGCG	22-0081	GGCTCGGTGGGTGTCCTGAGGGA	22-0081	TCCCTAGTCGAAAAACCCAGGCG	
22-0151	22-0151	TTGGAACTTATCAACATCTTCG	22-0151	TGTCACTGGCCAAAACATACCTAT	22-0151	TATTCCTGCTTGGGATCTCAGGATCAG	22-0151	CTGGATCTGAGATCCCAAGACGAAATC	
22-0161	22-0161	CCCAATCGACGGTCTGTGGAC	22-0161	CAAGCTATGCATTAAGATTATG	22-0161	TCCATTAAGAGAGCCCAAGATGCTCATG	22-0161	CATGAGGATCTGGGCTCTATCTTGGG	
22-0181	22-0181	TCACTGATGGCTATGCTGTCAG	22-0181	GTTCAAGCTGTATGACCCGTTA	22-0181	CATTAAGAAATTTGTCACAGTGTCCATG	22-0181	CTGTTTCTCACTGTGACATTTCTTTATG	
22-0191	22-0191	TCAAGAGATCTCTCTGCTCAG	22-0191	GAGGGCTCTCTTCTCTGTGGCA	22-0191	GTCAACACTCCAGAGGTGGGAACTG	22-0191	CAGATTCGCCAACCTCGGAAGGTGAC	
22-0201	22-0201	TCAAGTGAATCTCTGCTGCTCAG	22-0201	GGGGCTGACATTAATGCAATTC	22-0201	AGATCTTATTAATCAGTCAAGTGCATGG	22-0201	CCAGTGCATCTGACATTAATAGGATCT	
22-0211	22-0211	GAACTCCAACTCTTCTGCTATCT	22-0211	ACGACATGAGCAATGACAGGATAT	22-0211	AGATGAAGCAACAGCTTAACGACCGAC	22-0211	CTGGCTGGTGTAGCTGGTCTCATCT	
22-0231	22-0231	GTGACAGAGATGCTCAACAG	22-0231	TGTTTCTGTTGGAAAGTGG	22-0231	CTCAACACAGAAATTTGAAACATAAATC	22-0231	GATTTTATTTATCCCAATCTCTGTGTGAG	
22-0241	22-0241	GGAGAGGATGCGGACAGGATTA	22-0241	AGGCAATGTTCTCCAGTCTTAT	22-0241	TTCATTAATCAAAATGTGAGCCAAACCA	22-0241	TGTTTGGCTCAATTTGTGTAATTAATGAA	
22-0251	22-0251	CAATCTTCTTCTTCTCAACAA	22-0251	GTATTCGCCACTTCCAGTCTCTC	22-0251	ACAATCTTCTCAATGCACTACTGACTA	22-0251	TAGTCAATGTTTGGCATGACAGATGTT	
22-0261	22-0261	TATGTGATAGGTTGATGCTGGT	22-0261	GAATGGCAATATACCTCTCA	22-0261	CTCTCACTGCTCTCTCTTCTTCCATTAGA	22-0261	TCTAATGGAAAGAGAGACTGAGACTGAGAG	
22-0271	22-0271	OAGCTGTGCTATGTTGGGAGTAG	22-0271	GATTTGAAGCTCTGAGTTCAG	22-0271	AGACTCTCCCTGCTAGATCAAAATTTATGAC	22-0271	GCTGATAAATTTGATCTAGCAGGAGGTCT	
22-0281	22-0281	AGTAAAGGTTAACTTGTCACTCTT	22-0281	CAGTTCACGATGATGCCAGTA	22-0281	CTTCACTACCATGTATCTCATGCGGCA	22-0281	TGCCCATGAGAGATTTACATGTAAGTGAAG	
22-0291	22-0291	CGGGGTCTTCCATGTGTGGTC	22-0291	GGGGTCACATGTTAAACCTTA	22-0291	TCCAAAGCATGTGGTGGGCGGCA	22-0291	AGCTGGCCACCGGAGTGTCTTGGCA	
22-0301	22-0301	TGGCTGAGTTAGATGGGTGTAGCAT	22-0301	ACCAACCGACCTCGCAGCA	22-0301	GGGAGACTGTGGTCTGTCTGACGCGT	22-0301	ACGCTGCACAGCAGCACAGTCTCCC	
22-0311	22-0311	CTGCTCTTCCCAAGACTCA	22-0311	AGGCACTGCTCCACAGCAGGAA	22-0311	CAGCCACACAGACTACTCTCTCAAGAGA	22-0311	TCTCTGAGAAAGATGATCTTGTGGCTG	
22-0321	22-0321	CATGGCAGAAATCAGCAGCTT	22-0321	CTAGTCTGAGCCGATGCTTA	22-0321	TGCTACTGACACTACAGAACTATGGG	22-0321	CCCATATGTTCTGTAGTGTGCTCATAGAC	
22-0331	22-0331	CTGAGATGATGATGATGATTTAT	22-0331	GGACAGTCAATGATGATGATGATGAT	22-0331	TATGACTACATGTATGATGATGATGAT	22-0331	TGAAATTCAGTCACTACATGATGATGAT	
22-0341	22-0341	TATGATGTCTCTTCTCATCTCAG	22-0341	CTCAAGGCGCTGACATCTTA	22-0341	TCTCACTAGTATCTCACTAGGACAT	22-0341	ATGTCCCTAGTGAATCACTAATGATGAT	
22-0351	22-0351	TGATGGGTGTGGAGTGTGACAA	22-0351	TGCTCTTGTGCTCACTT	22-0351	AACATCTATTTAGCGCTTTGATCTCCA	22-0351	TGGAGATCAAGGCGCTTAACATGATGTT	
22-0361	22-0361	CAAGATGTGAGAGGACGTGCTTA	22-0361	TTCCGCTTGATTAATCTGTA	22-0361	TTCAGTAAACAAAGAGCGGCTGGTTC	22-0361	GAACCCAGGCTGCTCTTGTGTTTATCA	
22-0371	22-0371	TGAGATGTGAGAGGACGTGCTTA	22-0371	ACTGTCTCAACCTGGAATGTGAT	22-0371	CAGATGACTACTAGTAGCATGTACAG	22-0371	CTGTACATCTGACTGATGTAGTCACTTT	
22-0381	22-0381	AGCAACGCAATGATGACATCAATC	22-0381	TGCAAGCAATGATGACATCAATC	22-0381	TTTAAACATTTCTCAACAGATGTGCGCC	22-0381	GCAGCATCTGCTTGTGATAAAATTTTAA	
22-0401	22-0401	TTGGAAATTTGGGACACTTTTAMCA	22-0401	TTTGGAAATTTGGGACACTTTTAMCA	22-0401	CAGCTCTGACTGCAACCTCTC	22-0401	GAAGAGCCCTTAACAGACTTTTGAAGAT	
22-0411	22-0411	CAGCCTGACTGCAACCTCTC	22-0411	CCCAATACCTATGAAATAG	22-0411	GCTCTCAACAGACTCTGTAGGGGCTCC	22-0411	GAAGAGCCCTTAACAGACTTTTGAAGAT	
22-0421	22-0421	CCCAATACCTATGAAATAG	22-0421	AGGCTCTTGCCACTGATGAGAG	22-0421	CTTCAAGATTTGCAAGCTCT	22-0421	TGTCTTAACTTGTCTTGGCCACTGTTTC	
22-0431	22-0431	AGGCTCTTGCCACTGATGAGAG	22-0431	CTTCAAGATTTGCAAGCTCT	22-0431	CTTCAAGATTTGCAAGCTCT	22-0431	ATGCTGTGATGATCTTGGCCACTGTTTC	
22-0441	22-0441	GGGGGAGGCGACCACTGCTC	22-0441	ACTGAGCTCTGTGAGGCTCAATG	22-0441	TCTGAGCAGCTCTCTCTCACCAGCAT	22-0441	ATGCTGTGATGATCTTGGCCACTGTTTC	
22-0451	22-0451	TCTGAGCAGACTTAAACATCTT	22-0451	GAACAGGATTCACACAGCATCTT	22-0451	GGCTGTGAGGCTGGAAGGCACTG	22-0451	CACTGGATTTCCAGCTCTCCAGGCTC	
22-0461	22-0461	TTTAAATGCTTCAATTTTGGGTTA	22-0461	CTTCAAGGATTAATTTCCGCTCTA	22-0461	TTCGCTCTACAGCACTTCCAAACAAATG	22-0461	CAATGATTTGGAAGGCTCTGCTGCTGA	
22-0471	22-0471	AGGTGTGCACTGTCAACCTCAAGC	22-0471	AGAGACTGTTTADCAACAGAGCG	22-0471	TCCAGCCAGCAGGGGCGCATCTG	22-0471	CAGAGCTGCCCTCTGCTGCTGCTGA	
22-0481	22-0481	TGGAAGCAGACTGCACTGTA	22-0481	AGAGCTGTTTADCAACAGAGCG	22-0481	TCCAGCCAGCAGGGGCGCATCTG	22-0481	CAGAGCTGCCCTCTGCTGCTGCTGA	
22-0501	22-0501	CCCTGCACTTACTTGCCATATGAC	22-0501	AGTCTCAAAATATCTATGTGTT	22-0501	ATATGACTTTGGGCAAGCACTGTGAACCC	22-0501	TTGTTCATGATGCTGCTGCTCTGCTGAC	
22-0511	22-0511	TTTCAATTCATTAATCTTCTTCTA	22-0511	TCAACCTTACAGTTCCTGMAACC	22-0511	TAAAGTGTGTTGAAGAGACTTGGGAACAC	22-0511	GGGTGTGACCTCTTCCCAAAATCATAT	
22-0521	22-0521	TGAATATGAGACTTGAACCTGGA	22-0521	ACAGAAATTAACCTATGGGATG	22-0521	CTGGACCTCTCACTTAAATATCTGATGCT	22-0521	GTGTTTCCGAGCTTCTTCAACACATTTAA	
22-0531	22-0531	CATGACAGCAAGAGCTCTT	22-0531	TCTCTTCTGCTTCTCTCTAGT	22-0531	AGATCAGCGGAGCTTATGGAAGAACTTC	22-0531	AGCATGAGATTTTAAATGATGAGCTCAGG	
22-0591	22-0591	GGTGGCCAGCGGGGCAAGAGATTA	22-0591	CTTCTCTGCTTCTCAATC	22-0591	GGAGCGGCGGACACGGCTCTTGTCT	22-0591	GCAATGTCTCTCAATGACGTGGCTGATCT	
22-0601	22-0601	GAAGGACCCCAAGCATGAGGAGAG	22-0601	CAGTATGGGACAGGAGGMAAA	22-0601	CAITGGAACTGTGTGACTGCTGGAGCC	22-0601	AGACAGTCTCTCAATGACGTCCCATG	
22-0621	22-0621	CTTGCACACTTCTTGATG	22-0621	CAGTATGGGACAGGAGGMAAA	22-0621	CAITGGAACTGTGTGACTGCTGGAGCC	22-0621	GGCTCTCAGCTCTGACACGCTCCCATG	
22-0641	22-0641	ATGTTGATGATGATGATGATGATG	22-0641	TTAGCCAGGATGCTGCTGAT	22-0641	GTACACATATGCTTACGACCTCAAGAGAG	22-0641	TCTTGTCTTAGCAGCGAGGTCTGTGACC	
22-0651	22-0651	GAAGGATGAGGACAGAGGATGAGG	22-0651	CCCTGGGCTCTCTCAAGGCAACT	22-0651	GGGACCTCTGCTGCTGCTGCTGCTG	22-0651	CTCTGTGATGCTGATGATGATATATGTTAC	
22-0661	22-0661	TGCAACAGACAAATAAGCTACGAT	22-0661	GACAAACTTTGCAAGGATTA	22-0661	GAACAGGTGCAATAGGAACTGGATTTGGA	22-0661	AGGAGAGAGGCGGACAGGCTGCCCG	
22-0671	22-0671	GTGAATGGAGATGAGACATAG	22-0671	AGAAAGCACTCTGAAAGAAATAG	22-0671	TCTGTTGTGCTTCTGCTGCTGCTGCTG	22-0671	TCCCAATTCATTTTCTTATGACATCTTTC	
22-0681	22-0681	AAAGGCTGAGAGAACTTGAAGAGCC	22-0681	ATAATCCCACTCTGTGAAATCAG	22-0681	TTCGACACTTTGAGCCAGCATCTCTG	22-0681	GTATCAATGCAACAGAGGACGACAAACGA	
22-0691	22-0691	TGCTGATGATGATGATGATGATG	22-0691	AAAGGCTGAGAGAACTTGAAGAGCC	22-0691	TTCGACACTTTGAGCCAGCATCTCTG	22-0691	CAGATGATGATGATGATGATGATG	

Table II

Table III 627 single nucleotide polymorphism (SNP) markers

Note: In each block: First part of the first line, Name of the SNP; Second part of first line sequences length shown; G/A or alike, polymorphic site showing nucleotide sequences variation; Other parts, nucleotide sequences flanking the polymorphic site.

01T002 132bp
CACGTGTGAG GCCTTGCTCC CCACCTGTGG ACTCAGGGTC TCTTTCAC
G/A
GACTGCGGGG AAGGCAGTGG GAGCAGCAGG AATGGATGGT GAAAGGACAC AGTGCCCGCC
CCCCGAGTGT CCGAGGGTAG AGC

01T003 145bp
CTATAGCCCC TCTGAATGGT CTGTGACACA TGCATGCTTT CAGCTATTCT CTCTATAGCC
CTTCTGAAC
A/G
GTCTGTGACA CCATTATGCT TTCAGCTACA GTTTGCTTTC TCTGGTTTTT CAGTGGTGCT
CTGGGGAAGG CAGAA

01T006 141bp
AAAGAAGAGA GGTTTTTGGG GATATTTTTA ACACATCTAT AATCTTTCAT TAACAGCTAG
AAATTTAGAT TGC
C/T
GTACATAAGT GATAGACAAT GAAACAGAGA AGGCATTTCT GAGAGTCTCT CGGCTGTCAG
CATTGTG

01T008 147bp
ACTAAGGAGG CATCAACAAC TCTCCCAGCA GCTGATGGAG GATGGAAACC ACACAAGTGC
GGAGATTTC GGTGGGGACT TGGTGGGGGT CGTGTTCAGCC
C/T
AGGGAGAGAG GACGGAAATT CAGCAAGGAC GTAGAAGAGA GTGCTT

01T009 130
GTACGGTGCT ACAGGACCCA ACAGAGCCAG AGACTTGACC CAGGTC
A/G
TTTAGCCACC CAGCCCCAAG CCAGCAGGGC CAGCCAATGG GAGCCTGTGT CCCACCTCTC
GCCCCCACTC AGACTGTGCT CCC

01T012 138bp
CAACTTGAAG TAGTAGGTAT TGGAAC TAAG AATGATATAA ATAGAAATTA ACAATTC
G/A
GAGATTAGAA TAAGGTGCAG GAAATTACTC TGCAGTGTA TTTTGTGTTT CTCTTAATTC
AAGAGAGCTT GGAATGCTA

01T013 131bp
GAAATTCTAT CTCACCACCG TGAACTCTT CAGTTTCTA ATTGCTTTAT CAGCAGGGGG
TATAAAGGT
C/T
ATGAAAGCAA TTTCCACATG CTGTGGCTCC AGGTCTCTGG GTGTGAAGCA GAGCAAGCCT

01T014 140bp
ACAGCCTGTC ACAGAAGTCC TCTTTGGACC AGATAGGGCT GCCTCACAGG GGTTCAGTT
TGTCATTTCA
A/G

TTCAACAAGT CCTGAACACT TACTCTGTGC CAGGAATTTT GCTGGGCATT AGGGATCCAG
AGAAGAAGA

01T019 139bp
ACTGGCCACC TCTGCAGAAG CTAATTGTCC AGAGGAGGGA AAATACAAGT TTATAAATAA
CTAAATATC AGGTCAAGCA CATTGCAGG
A/G
AGCAAAAGTG GAATAGAATA ATGGGGCTGG GAGCTCCAGG AGGAAGAAC

01T020 147bp
AACACCTTGC CTGGCATATA GTAGATACTC AATAAAATCT CTGTTGGATG ACTGAGTTTA
GGCTGAGGGA GAGGGAGAAG AGGGAGGCAG GGAA
G/A
CAGGAATGTC TGGGTCCTTC TTAGGCTCTC ATTTGAGTGT CCTCATCCAT TC

01T023 131bp
AGATTTTCTT GACCGTCTTC TTATTCAGAA TTCATCTTAA ATAAATGTCA CCTCCTCAGA AT
A/G
GTCCTCCTTG ATTGCACTGG CCAAAGCGGC CACTCTGCTC CCCAAGTCAC CGTTGAATCT
ATCCTTTT

01T025 138bp
AAGGGATAAA CCTCACTGAC TTGGAGGAAA TCAAGAGGAG TGAGCACAGC ATCAGAAAGC
CCCCTGGCCC CAGACTGCAC CC
G/A
CTTTCCTGGC CCTACCTTGA AATCCATCAG GTCTGCGTTG GACACGGCAT TGTAC

01T028 146bp
CCCAGCGGGA AGCTGTTGAA ATAGTTCAGG GGAGACGGGA GAGGTTCTGG ACCAGGGCAG
GGCAAGGGCA GAGGGGAGGG TT
C/T
AGGACCTGGA GCTCAGGTGG TGCTGATGGA GCAGAGAAGG GAGACAGACC CGCATGTGCT
TTC

01T029 108bp
AATTTAGGCC TTTATGTAAA TTCAGAATGA TACAGATTTA GACTTTATAT AAATTGCCA
A/G
TAAGTGGCAG AGTCAGGTCT TGAACCCAGC TGCTCTGAAT TTAAAAGCCT TTGCCCTC

01T032 101bp
CAAAAGACCT CCAAGTCTTA AAAAAAAGA CCTCAAAGGC CTAAATCTGT TCAAAGCTTC
A/G
AGGTATTCCG CAAGGATCTC CTAAACTCTT TTTTGTCTT GGTGGTATGA

01T035 RsaI
GTGCTCATGA GCCGCACGGG GCCAGCGCTG GTCCTGGGAC GGGT
A/G
CGGCCACCGG GGGCGCTGCT CAGCGTGCCC GTGCTCAGCA GCCT

01T037 122bp
CCATCAGGTA ACTGACAAAC TCTAAGGAAG CATCTCTGTT TTTCTGGCCC TGTACTAGGT
TCTGGAAGG
C/T
GGTGAGCCAG CAGGCAGGCC TGGGACTGGG AAGCCAGCAC TAGGGCTCAG GG

01T038 130bp
TCTTAGCAGG GGAACAGCC TAGGCAAAGG CCTAGAGGCT GGAA

Table III

A/G

GGGGTAGGTT TGTATGAGCC ATGGTGAACC AAAGTGTGAG AAAGAAATGG CAGGAGAGGT
TTGAGTCCGT TAAGAGAAGC CTTGA

01T039 130bp

CTCTCTAGTA AACCCGATCA CCTCCCACTG GCATGTGCCT AACACGTAGG AAGTTCTCAC

A/G

ATGCCCTATT GTTAATGATG GATGACTCTA ACTATGATAG CTAATATTTA TTGAAGGCTC
TGAGAAGCC

01T041 149bp

TCTCCAGTGA GTCTGGGGGC TGGCAGGGTG ATAACACGAG GCCAAGGCTC AGAGAACTGG
GCCCTGGTTC CTAGGCCTGG CT

C/T

TGACATTAAA AGCAGTATGA TCTTTGTTTG ACAAGTTATT TCACTTCTCC AGTCTTCAGT
TTCCAC

01T042 127bp

CTCACTCCCT CAGGCCTCCG CCCAGTGCTC TTTCCACAG AGGC

C/T

TACCCTGACC ACTTGATCCC AAACAGCCCC TGCCTGTCCT CCCTTCTCCC TCCCATCCAT
CTGTTCCCTGC ATCATCTTCC TT

01T043 113bp

ATTCTCGAAC TTTCACGCAC AGAAGAATCA CCCAGAGGGC TTGTGAAAAC ACAGA

T/C

TGCTGGGCCC CAGGCCCAGA GCTTCTGATC AGTAGGTCTG GCCTAGGGCC TGAGAAT

01T046

TCTGAACACC CGGTTTATAG TCCCAGTCCT GCCACTGTAG GACATTGAAT AGGTGATGTT
ACTCATCTGA AATTGTATCT

A/G

TTTTGATAAC ATGGGGATAA TATCTCTTCT CTCTACTTGA ACAATGAGGT AACACTGATG
ACC

01T047 147bp

CAGAGGGGTT GCCGTTGCTC CTTATCCTCC CATCATTTGA TAATGTCAGT TTTTTTTTAA
ATTTTAACCA TTCTAATAGG CATGTGGTAG TATCTCACTG

C/T

GGTTTTTATT CATGTTTTTC TAATAACTAA AGATGTCGAG TGCCTT

01T048 140bp

CCACACCCTA GAAGGCTGTA GAACATGAGG ACATGAGCCA TGTAGGACGT GAGGATGA

T/C

GCCAGGGTTC CAGTGCAAGC TGAGACTTAA GGGTACCTTC CAAGAAACCA GGAGGAAAGA
GCGCAAGGAA CTGGAGTTTT T

01T051 130bp

CTACCCTGCC TCTGGGCCTT GACCTGTGCC CTCTTCTTCC ACAGCTGTGA TTGTGGGCGG
GGTGGTGGG

C/T

GCCCTCTTTG CTGCCTTCTT GGTCACACTG CTCATCTATC GTATGAAGAA AAAGGATGAG

01T054 133bp

TGAGATGGCC CAGACTCCGT GCAAAGGAAG GCAGGATGAG GAGGAAGTGA CC

A/G

TCTTCGTCAA GGTGCACAGA GCTGCACAGC AGCCCAGATG GCTCTGCTGA GAAGACACCT

Table III

CATTTGGAAG TAAACACAGGC

01T055 118bp
CCTGGGGCCG GTGACAGGAA AACTAGACCT GAAAGTGTGA GAGGAAAGAG AAGTTGCTTG
AACTCAGAGA G
A/G
CCTCTGTGGA GAGGGCCATC CTGCAGGAGC TGAGATCTTC CACTAA

01T056 122bp
CACAAATGGGA ACAATAAATC CAACCAGAAG GAGGGCCATG TGTGTGAGCT TGACAGTGCA
A
T/C
GCATGGGAAA AGGAAGAGGG CGGGTCTTCC TGGGTACCA ATTCACATCC ACCACCATTG

01T057 137bp
CCCATTAGCC AATGAACAGC TTGTTTCTCT TCCTGAAAAA AGGATAGATC TTACA
C/T
TCCCAAAGAA TCAGAGCCAG ATAACAGCAA CAACTTATT GATCAGTTAC TATATGGTAG
CCATAGTTTT GTGGGTTTTT T

01T058 142bp
GTGTTCCCGG TCGGCATATG ATGAAAAACA TGGGTTTGTT CCTGGGCTAG GTCTCGGTCC
GAAGCATGAA GGGATTA
C/T
TAAACCCCTC CCAATTACTA TAAAATAAGA CAGTAATGGT TTAGATTATC CTTTTTAGTG
GTGG

01T060 130bp
GGACTGCTAC TACACAATGG AGGTAAGGAA GATTATGTCT GGAATAAAGA AGATCC
C/T
TTAGGTTATC TCTTAGTATT ATCATGGCCT ATGATTAAGA TCAATGAAAA ACCAGAACAA
CTCAATCCAG GCA

01T061 125bp
CCAGCGTTCT GCAAGGGGCT GGGTAGAAGG GGCTGGCATG GGCATCTGGA ATCCTTCAGC
CTAGTCCTCT GGC
T/C
CGGTGATGAA AGCCCAACCA CTGTTCTCAG ACCAGCAGGG ATAGTCTATC C

01T062 142bp
AAATGTGGTA CATGGTCTTT GTAGTGATGC CTGTTTTTCA AAATTTCACT CTACAAACAA
CCTCACCA
T/C
GAACTGTTGT GAGAACTGTG GGAGCTATTG CTATAGTAGC TCTGGTCCTT GCCAATCCCA
GAAGGTTTTT AGT

01T063 95bp
ATTCATCACA TAAAATGCAA CTACCCTGTA ACTCACATAT GTAAAT
C/T
CAATAGCAAG AACATTCTG AGATTCAGCA GTGGGATTTT AGAAAGCT

01T064 146bp
GTGGTCCTAC ACAAAGAAAC GAATATTGGA AATGGCATTT AGAAAGCATG TACTACACGT
TTTCTTATAA TTAAATCTT TCAAAAAATA TTTGACGTAA
T/C
AAATAAAAGT AATAATAATG AATCACAAAG GTTATAGTGC ATAAA

Table III

01T065 141bp
 GCCACTCCTG ATGGATGATC TTACTTGCTT TGCCAATGAC AGGAGTGAGA TGACCCATTT
 CTAGCAAAGC CATGAGGCCG TATCTG
 T/C
 TGGAGCTTCC AGGGGAAGAC TTCCTTGCTT TAGAAGGACA CAGAAAAATC TGTC

01T066 148bp
 TTGAAAGTTC TGGTGTATAG CCCAAAGGGG ACAGACAAGA AACTTAAGAG TCTG
 A/G
 AAGGGGTAAC AGGGGCTTAC GTACTTCTGT TTCTTTGATC CTTTATGAGT TTTCTCTGTT
 TTTTCAGCTG ACCTTCCCT TGAGTGA CTG GAG

01T067 143bp
 AGAGGGATAC TTGTAAACTG AAAAGGCTGA GCCCAGAAGA TAATACACCA ACCAACCTCT
 TTCTTA
 C/T
 CATTTCTAGG CCCAGTGTT ATCTGACTAT TCACCTAAAA TTGTAGAGAC TCGAAGGGTT
 GTGGCAAGAA CACTGG

01T068 125bp
 TACAATGCTT TTCTTCAACA ATAAACAGCA AGATCAACAC ATGTACT
 A/G
 GTATAGCTGC TTAGCATTTT TAAGGGAAGA ATAAATTATA TGGCCAGCCA GCTAGCAAAA
 TAGAGTGAGC TACCACA

01T069 131bp
 TATCCCTCCT GCCATCCGTG GAAAAATTGT CTTCCACGAA ACTGATCCCT GGTGCCA
 G/A
 AAAGGTTGGG GACCACTGTC TTAAAGCATG CCCATAAGGG TGGGTAGCTC ACTGGACATC
 TACTGAACAA TTT

01T070 131bp
 TTGTCTCCTC AGGTAGTGAT GAATTAGTTG CTGTCACAAA AGGAGGGAAG TAGCACCCAA ATTAA
 A/G
 TTGCTTAAGA GAGGAAATGT ACATCTTGTA TAACTTAGGG AGCGAAGAAA ATGTAGGCGC
 GAAAG

01T071 141bp
 GGCCCCATT CCAAGAACCA CGCTGGGCCA GGTACATGG CTCCCTTGGA GCTTTGATGG
 CACTTC
 T/C
 TTGGGAAACA GAAGCTGAAT GTTTAAGAAG CATCTGTCAT TATGGAAACG AAGTTGCCAG
 GCCATTTTTT CTTT

01T072 146bp
 TTGTTCTGTTA TGTATCACTT CTTTAAAACC TCAAAGGCAG GTTGATCAGT AACCAGGAAG
 AATGGATCTT TGAATTTCTG AATTCTTG
 T/C
 AGTAAACTT TCCGATGTCA TCCAAATCCC ACCCGAATTT CTTTTTAATT GAAAGA

01T074 102bp
 ATTAGCACGT CAGCTTCTC TTGTGGTATT TATGTGTTTA TATAACA
 T/C
 AGTTCATTGT TCCCAAATGT TAGTCAACTC CAËCTATAAA TCAAGCCCCA AATC

01T077 124bp

Table III

CAAGAGAGGT CCCACCAGGA AATATTATAG TCAAAGTGTG AAAGGCCAAA GGCAAAGAGA
AAATCTTG

A/G

AAACAGCAAG GAAGAAGCAA CTGTTTACAT ACAAGAGATT CTGAATAAGA TTGTC

01T079 127bp

GATGGGAGCC AAACATCATC CTTTATCAG GAACCCACTC CTGTGATAAC TAACCTACTC
TCATGATAAT GACGGCAGG

A/G

CCCTCATGAC CTAATCACCT CTTAAAGGTC CTGACTGTCA ATGCTGT

01T083 129bp

CCTCTTATCT GAGAATGACC CTTCTCCCC AAGGAGTCCC AAAAGGTGGG CTTCTTTGTT
GATTTAGAGA

A/G

TCGATAATTC AGTAAAGTCC CAAGTAAATG GCACAACACA AGCTCAGA

01T084 142bp

CAAAGGGACA AATACTGTAT GATTCTACTT ATATGAGGTA CTAGAGTAGT CAAATTCA
C/T

AGAGACAGAA AGTAGAATGG TGGCTGCCAG AGCTGGGGAA TGGGGAAATG AGGAATTAAA
GTTTAATTGG CAAGGAGTTT CAG

01T087 137bp

GCTTCAGAGC TCTGCCAGCT GCCATTCTAC AGAGGCAAGC CCCTCCGGCC CCATCTGGCC
TCCCTGACCC AGGG

C/T

GCTGGCCTCT GATTGCATTC CCCTAGTGAC AGGGAGCTCA TTAGGGCCTG GGGCTTTGGG
GA

01T088 145bp

CAACCCCAAG ACTCCCAGGC ACATGGGATG GATGTCCAGT GCTACCACCC AAGCCCCCTC CTT
C/T

TTTGTGTGGA ATCTGCAATA GTGGGCTGAC TCCCTCCAGC CCCATGCCGG CCCTACCCGC
CCTTGAAGTA TAGCCAGCCA A

01T089 146bp

ATTTACATGC ATTTAATCCA CGCAGCAAAA TCCTAGGAAG ACAGTATTAT AGACCCTATT
TTGCAGTGAG TAGACTGAGA CCTAGAGAGG C

C/T

GAGCCACTTG TTCAAGGGCA TACAACCTACC TGGTGGGGGA ACAGGACTGG AAAC

01T090 147bp

CAGCATGTTA TAAATGCTAT ATGGAGTAAT AAGTATGGTA AGAGAATAAT GATTGAGGGT TGGG
A/G

TTACAATTTT AAATTGTGTG GTCAGGAAAG GTGACATTTG AGCAGAGACT TCAGTGAAGT
GGGTAAGTGA ACCATGTGGA TC

01T091 147bp

ATTTGGAGCC ATAAACATA TCTAACTAA TTTAAAAGAA TGGAATTCAT ATAATGTTTA
CTCTCTGGCC ACAA

C/T

GGAATGAAAC TAAAAATAAG TAACAAAAAG TTACCCAGAA AATCCCCAAA TACTTGCAGA
TTAAACAACA CA

01T094 112bp

TCGAATCTCG CCCAAAGTGA CGAATAAATC CGGACTCTCA GCAACATGGG CTATAGGGAG GATCC

Table III

C/T
TAAGAATTCC TCAGTGACCA GATAACTCTG TGCATAGACC AAGGTA

01T096 116bp
TCAGTGCCAG AAAGATGTGG CTTAAGTTCC TGCGACTCCC TTAATGTGGA GCTCAGACAC T
T/C
GCCATGGGGA GAGCCAAACT GCCTTCACAG CACTAGATGC TCCATAAGGG ACCA

01T097 148bp
CAGGGTCCCT TTCCGTAGAG CCGCCAAGTT CTGGTTCCTT GTGGGTCCCG C
C/T
ATGCACCTTC CATCCATATG TGCACATACC AATGTGCAGC TCTTTTTATT CATGTAGTGG
ATTTCGGATCA CACATATAAT ATGCCTGTGA CGACTT

01T098 134bp
GGCCAAGGTA TAATCACACT GGTAGCTGGA AAGCCTTCTG GGCTGGGGTG CCATAGGCTG
T
A/G
TTTGGGTTCC AGTTCCAGCG CTGACTTTGC TCTATGATTC TGGACAAGTC ATCGCCCTCT
CTGGGCCTCA GT

01T099 145bp
CCATTGCTGT GTCCAGGGC ATTTGGCAGC ACGGCTGGGT GGTTGAC
A/G
AGGCCAGGAG TAGTATGTGC AGGCACAGGG TGGGCGTGGC AGCTGTCACA TGGCAGAGGA
CCCGCAGAAG CTGCTGATGG CTGGAAGGTA ATTAACA

01T102 130bp
AAGAAGCCAG GTACCAAAGA GTACATACTA TGTGAATCCT CTTAACATGG AATTCTAGAG
CAGGCATAAT GGTTCATAGT AC
A/G
TAAAGCAGAC CAGCGGTTGC CTAGGGTGAG GAGTAGGTGA TGGGAGG

01T103 148bp
GACAGGGTGA TCAGGACAGC TTCTATAAGA AGGTGAGGTA TGAATTAATG C
C/T
TAAAGGAGGG GTGAACATGA GCTAGGCCAA TTGCAGGAAG AAAGGGTCAC CAATGAAAAA
GCACAAGCTA GGATACATCC CAGGAAAGAG CCAGAT

01T104 109bp
CTGGGAAGAC GTCTCTTCAA AGCTATTTGA AAGAACTGTG CTTTA
A/G
GAGATAAAAT ACCTAAACAA GCAAATCCTC AATTTCTTTA CACAGACTTT CTGTCATTAG
TGT

01T105 140bp
AAATGTCTGC AGTCTGGCCT CTGTCCCCTT GATGCCAAAC AAAAC
C/T
GCCCTGCCCA AGGTCACTGT TGTAATCTA AATGACACCC CTCAGCAGCA GTGGGAGCAT
TCTGTCTCTG TGTGTTCTCT GACTCTGTGG CCTC

01T108 134bp
GGATGAGAAG GAAACAAGCC TGGTGAAATG GAATGGTCAG AAAAGCCTCT
C/T
TAGCATAGTA CTAATTACGG GGTAAATTTT ATGAGGAGCC TGATTTGGAA GTTCAAAAGA
GGCGAGAAAC TAGACAGAAT GAA

Table III

01T109 107bp
 CATTGTGTG CTTGTCTCCC TCAAGAATAG GGACTTCTCA AAAATCAAGC TACATGCTGC
 AAGTGCTTGT ACC
 C/T
 AGAGCTCTGA ATCTGACACA AAGTAAGGTT CATACGCATT CAA

01T111 122bp
 GGCTTATTTG ATGGAAATGG TAATAATGAT AATAATAACC ATGAACCTAC TGAATATGAA
 ATATATTAAT AA
 A/G
 CCATCTTAAA ATGTTATTTA CTCTTCACAA CAATGAGAAA AATGTGTAT

01T117 144bp
 GTCTCCATCT CTCTTAAAGG AAAAAAAGAC GACATTACAC AGCAACATGA TTATTTAATT
 AATAGCTTTT CC
 C/T
 TTTGATGCCA GTCTTGTTTT AGTTATAATA AACTAATAG GTATATCTGT CAAAGGACTT
 ACAAATAAAA G

01T118 126bp
 TGCCAATCTT TCTGGCAAAA TCAAAAATGC TTCCAAACCC AGGGAAGCAG
 T/C
 ACTACTCTGT GTGAGAAGTT CTGTATAAGC ATAGCTATCC CTAAATGCAG GCTAGCAACC
 ATCTCCCATC ATAAA

01T119 143bp
 GCCAGAGGCT GATGGCAGTG AACAAAACAG ATGAGTTATA GCTTTAC
 C/T
 AGTTGGTGAA AAAGAGAGTT TTTAAATAAA AAGTTATACA ACTAGATATA ATTATAAATC
 ATGTTTACAG AGTTATGTGT GAGAATTAAA AGGGA

01T120 142bp
 CCTATAATCC CAATGCTTTG GGAGGCAGAG GTGGGAGGAT TGCTTGAGGG CAGGATTTCA
 AGACCAGCCT GGGCAATATA GCAAGACCCC ATTTT
 C/T
 ATAAAAAATT TAAAAAATTA GCCAAGAGTG GTGGCAGGCT CCTGTA

01T121 120bp
 GAGGCAGGGT AAGCAGGATT CAGATTGGCG AGTTGGAATA CTTTCAGCAG GCTCAGGGCT
 GGCTGTCTTT AGTTGTC
 C/T
 GGTACCTGGG CCTGGGGTGA TTAGAGGCGG GGAATACTGG CC

01T127 140bp
 GGAGCTGCCC AGAAACAGCC TTGTGGGGTG GGGTTGGTGT CTGACCT
 T/C
 CCTCCCCGGG GGCCTTCGCA GGCTTCTCTG CTGGTGCTTC TGTGCCTGTG GGTCTGGATT
 CCTCCAGGGC CTGATCCTGG GTGCAGATGC AG

01T128 142bp
 TCCCAGGGGC TTCTGTGGCC TGCTGAGGCG CAGTGGGGGA GGCTGGCAGA GGCAAGAGGG
 CAGGGCCTGA GGGATGG
 A/G
 GATGGGAGGC TCTGCCTCTC ACATGTCCTG TCCTCTCCAG ACCCCAGGGC TCCGTCCTCT
 GGAC

01T129 141bp

ACCCAATATG CCAGTTAATA CTGACATTTC CAGTGGGAAG GGAAGAGGTG AGAAGATAAC
ACCTGAGTGG GCTGATGAGC C

A/G

GAACAGTTTA AGTGGGGGAA AGGTCTGGCA TTGCCTTAGA GCTGGTGACC AGACTCCCC

01T131 133bp

CCTGTTATTT TCCAGAATAA TCAGTGATAC TCTGTGATAT TGATAATCTA CCTTGTGGC
CCTTACCAA

A/G

TTACTGGGTG TGAGTAACAG CTGACTGTAG CTCCTTTCT CTACCCTAGT GCTCTGGAAG
GAG

01T133 126bp

AATCTACCAA TCTGACAAAG GGCTAACATC CAGAATCTAC AAAGAACTTA AACAAATTTA
CAAGAAAAA ACAACAA

T/C

CCCATCAAAA AGTGGGCAAA CAATATGAAC AGACACTTCT CAAAAGA

01T135 129bp

TTAAAGTCTT TTATGCCTTC CCACCCATCA TTAAAAATTA ATAAATTTTG TCACTCAGCC
ATTTACAAAA TAATCTGATA

C/T

TACAGATTAT TTTATTTCTT TCTACAAGAA AACCATATCC TATTTCTT

01T137 148bp

AAAAAGGAAA CCACCTTCTT ACCAGGGACC CTTAGATCGA CCCCAGGAGG AGCCCTAGAT
GCTGTTCCC

A/G

TACCACGCCC TCTCCAGCGG GAAGTAGCCA GAAGAAGTTG TTGCCCAATT CCCCCTAACA
GCAGTTAGGG ATTCCATT

01T138 105bp

GAAATGATTC ACACCAATTC ATGATAGAAG GTTGCACTTG C

A/G

GAGGGTTGGT GTATTAGTCC ATTCTCACAC TGCTACAAAG ATACTACCTG AGACTGGGTA ATT

01T145 149bp

GGCAGCTGGA GGTTAAGCAT CTAAGATTAA TTCCTGAACA CCAACATAGA AAGGCCAC

C/T

AAGGGAGTTG CTGCCTGTCT GATCAGGAAG CTTCTGGAGT CAGGAGCTGC TTCTTTAGTT
CCTGGTTCCA GGATCATCCC AGCTCTGCTG

01T146 127bp

ATGTGTTAGC TCCCACTTGT AAGTGAGAAC ATGTGGTATT TGATTTTCTG CTCCTACATT
AATTGCTTA GGATTATG

A/G

TCTCCAGCTA CGTCCATGTT GCTGCGAAGG ACATGATTCA TTCTTTCT

01T147 140bp

AATATGATGA AGCGTAGTGA AACACATAT GTAAAATGTT ATTTACA

A/G

TGGCAAGTAC TTGAGATACA TTCAGTAATG AAGGCTATCA TCATTGTTAA TGGCAGGAAT
TTTCAAGTGA GTCATTATGT TTACATGCCA CA

01T148 102bp

AGGAAGGAAT AATAGAGAAA CTTACCCAC TTCTTTGATA AGTAGGACC

G/A

Table III

GACTCCATGA GCCATTGATT ACTTCTTGTG TCAGACTGGC ACATATCAAG GA

01T150 100bp
TCAGAAGAAT CGTTTGAACC CTGGAGGCAG AGGTTGCAGT GAGCCGAGAC AGC
A/G
CCATTACACT CTGGCCTGGG CAACAGAGAG AGACTGACTC AATAAA

01T151 126bp
GTACATTGGC CCCTTTTATC CATAGCTGGA GTGGCTGGGA CACAGGACAC CAA
G/A
TCCCTAGGCT GCACACAACA CAGGGACTGT GGGCCCAGCT GATGAAATCA GTTTCCTCCT
GGGCCTCTGG GC

01T152 134bp
TTCTTCTAAC TTCATACTGG CTTGTTTGTG AAAGAAAAGT CTTTGAAAAG GCTACCTG
C/T
AGGTGATAAA GATTTTTTAA GTATTCTTTT CTTCCTTTTT ATTAGAGAAA ATCCAAAGGG
AGTTTTAAAA TTTGT

01T153 141bp
ACTGGATTAT GCTCCAGGTA TCTGACAGGT TTTCAATACT ACTA
A/G
TATGTTTATT ATAGCATAAA AGGGCAATAT AAAAATAATT AAGAACATCA ACTTTATAAT
AAACAAGACT AGATATTGAA TCCTTGCTCG CACTTC

01T154 117bp
CCATTCTTCC CGTTAAAATA GCAAAATCAA GGATACTAGA ATAATGTATA ATGTGTTCAA
CACTAAATCG
C/T
ACCTTCGAAT TTATATACAG TTTTAAAGAC ACTGACCCTA AGGAGA

01T155 149bp
GGATAACCTG ATGAAATTCA AACTTCTCTG AGTATCCATT TCCTTATCTG CTTATTCAA
C/T
TGACTAGTCA CCTCCTCTCT TTGGATATCT AATAGGTACT TAACATTTAA AATGCCCCAA
ATTGAGCTCC AGATTATCAC CATTCCCCT

01T156 130bp
TCCTTCTCCC CTGGTGTGG GGCTTCTATT GTGAGGTGAC CTCTGGCTG CTCCCTTATG
GGTCCCAGGA CCTAACCACA GTTG
A/G
CCAATCATAA TCCATCAGGC CCAGTTTGTT CAAATGAAT TGCTC

01T157 135bp
AGCATGTTTCG GATTTCATGA CTCTTGTTGGT TTTGTTCCCTA GACAGGACCT ACCAGGGGAG
CCTCCTGCAA ATGAG
G/A
TGGTCTTCCT TTTCTACTCA TCACATTCTA TGCCTGCCCT CTCTAACCTA CATGGTATA

01T159 139bp
GTTGAGTCAT TTGGCCTCCT TGATCCTCAC GTAAATTGTG GCATTATTAA AGTT
C/T
GGTCTACATC AAATGGTCAT TACAAAAATT CAGTAAGTGT ATAAATATAC TTTTAAACT
AAAAAGCTCT CAGGAGGCTG AAGT

01T160 147bp
CCCCTATGTC CCACAAACCT GCCAATCTCA GATTTCTGTAT CTCAGTTAA GATTCCTTCA G
A/G

Table III

TTTTTAGTTA TTCAGGTTAA ATAATCTTTG ATCTGTATCC TCTATTAAGT CCATCAGAAA
ATCCTGTTGG CCTTTCAAAA TATAT

01T162 136bp
AATTAGGTTT GAAAAGGGAA ATAGTAGAAT TAGAGTTGGG TTTAGAAACA AAATTAGTCT
TGTAATAGTA ACTATGCT
C/T
TTCTAGAGTG AGGCAGTATA GTCATGGAGG AGAACTGCCA AGGGATTATT TTAATGA

01T164 122bp
TTAACTTGTT CACGTAAAGT CCATTTCATAT ATTTTGAATA AGGTATAGAG GAGAGTTTTT
GAGTGACTCC TCACTC
G/A
TCTGAAGGTC TGTGACCTAT GAACTGCCTC AAGGCTTTCT CTTCA

01T166 138bp
CACATTTCTT TTCCATGTGG TATGTGGTGA AAAACAGAGA AACAATAAAA CCCAAGAAGT
CTTATTATTA TGACTCCCTT CTTAAAATGC C
C/T
AAAGAGCTCA AGAATAGTAT CTTGGGAAAA TTACTATGTG TATGGA

01T167 105bp
ACAAAATTTT AATGCTCTGT GGATCATTAT CTGGCAACAG ACCAACAGCA GA
G/A
CATAAACAT TAACAACATA AAGCGGGTTC TGAGTCCTTG GAGTTTCTAA TT

01T169 131bp
CATACAACCT CCCAAGACTA AACCAGGAAG ATCAAATTCC TTACTAGACC AATAACA
T/C
GTTCTGAAAC TGAGACAGTA ATTAACAGCC TACCAACCAG AAAAGTCCAG GACCAGATGG
ATTTACAGTC AAA

01T171 133bp
GCAAAGGGTA AGAAGAGGAA GTGGCTTCCC TTAAGTTAGA AGCTGTTTTT ACCTATGGGC TG
T/C
GACAATGCAC TGGCCATGTG TTCTAGACCT AATCTGGGTG AGTGAATAAC TGGGAGGATG
TGGAACCCAG

01T172 148bp
ACACTCCAGG CCTGATACTT CTGGTGTTAA GCAATTTGCA AAATGATATA CTAATGACCT
TTCAAAAAGT TATT
A/G
CCACATCTGC TCTTTGTCAA GTGCAAGAGC CTAGTATATA GAAAATAATA TTAAGCTCCA
AGTGAATACA AGA

01T173 148bp
TTATAGAAGA TCCCCATTGA CGATGCTTTC AAGTTGAAAG AACATTTAGA TAAGCCATTT
GATATAGAAG TGACTTTTAT TTCACGGTCA AAACAATT
G/A
TCAGCCAAAG AAAGTTCCTA ATTTTGTGTA TTTGTGCACC ACAGTAAAT

01T174 140bp
AGACAGTTCA CTGTATTCTT CCCCCAATTC CTAGAAGAGT AGTAAGGGTC TTAAGGCGGG
AGAATGAGAC CTCCTGAAAT
A/G
CTTATGAAGC CTTCCCTTAT CAAGTACTCA CAGCCAAATA TTTTCAAGTG GCGTTAATT

Table III

01T176 147bp
 CAGCTGAGGC ATTAATATTC ATTGGATTGG GGGGGTGGTT CCAAGATGGC
 T/C
 GAATAGGAAC AGCTCCAGTC TACAGCTCCC AGTGTGAGCG ACGCAGAAGA TGGATGATTT
 CTGCATTTCC AACTGAGGTA CTGGGTTTCAT CTCACT

01T178 134bp
 CCTGTTAATA GCCACTACCT TCTTTTCACA TATCACACTT CCGCTTGCTT GTTAACATTC
 CTCAGTTTTTC ATTTATGG
 C/T
 TCAATGAGTC TGTTTTGCTT TACTTTATTT TAATTACTAT AGAATGTACT GGTAACCTTC TGATG

01T180 119bp
 TACCAGATTT GAGGCTCAAT ATCTACTTCT GAAGCTGGGA GTTGCAATCC
 C/T
 TGAGTTCACC ATTTTCTTTC ATCACTTTGT CCAGTGAACCT TAGGACCAAC CAACCAACTT
 TGTTATGT

01T182 139bp
 CATGCCTTTG TCAGGAGGCA TTCCCTACGT TCAAGTCTTA AGCATGTGTC CTGTATAAAA
 TCAGTCTTTA GCGTCTCCCA AAAGAGCTAT CACTT
 CCT
 C/T
 CTTTTATGAA CTTGCTGTAT CTTGTCTCTT CACTTGAGCA CCT

01T184 129bp
 ACCCAGCCTA GGGCATGGCA CGAAGGAAGC ACTCATGGGG CTTGGC
 A/G
 CATAGTGGGA GCTTGCCCAG TGCAGGGCCT GGCTCTTGCG TGCTCAGGAA ATGTTTGCTG
 AATGGAATTT CAGTGGAATG GA

01T185 134bp
 TTCAAATTGT AGATCTCCCC CTCCTATCTT CCACCCATA GCTAAGAAAG GAAACCCAGG
 GATAGAACTA ATTGAACCTT ATTAGCCAG
 A/G
 GGCAATCGAA CCCAGTGCCA ATAGAGAGAT GGACTCCCAA TTAG

01t187 145bp
 GCTGCAATGG CGTGCTGTGC TTGGGGGCAT GAAGTGTGCA GGGGTAGGTA TGCTGGCCCT
 GAGACTTTCC CCCGTGAGAA TTTCATTGCC ACAGC
 A/G
 CCAGTGGGTG GATCGATAGC TTTAGGAAGG TGAGGTTTCT TTTGTGGAG

01T188 143bp
 TAAAGCTGTA ACAGTTAACC TCTTCCACAT GCAGCATCTG CAGGCTGCTT CCCTTGACAG
 CAGTTTACAG TCTCTCTGTG
 A/G
 TAGTGCCAAA CTCTATGACC CAGGCCAAGA GTACAGTGAA TTTGTCAAGG CCACAAATTC
 AA

01T189 140bp
 CCAAGATCGT GCCATTGCAC TCCCGCCTGG GCGACAAAGT GAGACCCCAT CTCAAAATAA
 GTAAATAAAT AAACA
 G/A
 AAAAGAATTT CTTAGACGAA ACCTTGTGCC TTTTGTGCTC AGTTGGATAG GAAGTGAGCA
 TCTG

01T192 148bp
 AAACATTTTT AGAGGCCAAG TGTTCATGTT CATTCTTTAT CCACTACAAT CATATACATC
 AACTTTGAAT GGAGTTGTTT GTGATTGGC CTCATTA
 A/G
 GCTAAAATGC TTATGAAGAT AGATCTGCGG TTTGAGTAGC TTCAAATTTA

01T194 135bp
 AAGACTTCTG AAGCACCAGT ATCTGAAGAG AAAGCAATGG AACACTGAGG AGAGATA
 C/T
 GAAGAAAGTG GGACCATAGA GGCAGAGAAA ACCATGAATG ACTATGCTTA TACAAGCCAA
 ATGCAACATT TCAAGAA

01T195 132bp
 GTAAAGGGAG TGGCCTGTTC AATATGGGAA AAGACTTGCC ACACATTAAA GCATTTTTTC
 A/G
 TCTTATAAAA TTGATGTATT CTTGGAAAGT GTGTAAATTC ATTTTACATG AAGGGAATAA
 TTTTCATGTAA AG

01T196 142bp
 TGCAAAATCT TGTATTGCTT GACTACCCAA GTATTAAGTAA AAATAGTCAT GCCCATCAGA
 CACAGGCAGA GTTTATATAG TGAAACAAC T
 A/G
 AAACAGAGTT TATTAACAGC AAATATTCTT AACTCCATA GCACAGGAGT

01T198 116bp
 TGGCATTATG TGCCTCTTGA TGTGATGCAC TAAAAAGGAT ACATCATAGA GTATTAAGGC
 CAAATATGCA
 C/T
 AGATGAATTT AATCAGGAGA AAGCAATCAC ATAAATTGAG GAAAT

01T200 138bp
 TTTACATGAT GATGACACAA AACTGTAAA GGACCTCTGG GTTACTTGTT TATAAGCTAG
 TATTTCTTGA ATCAATTT
 C/T
 TCTGATCCCT AGATATTTGG TAGGTGAAGT CATACTATA TATCCCCACA CCCTAGAAC

01T202 139bp
 CCTTTTCATT TGTCATTGTC TATCACTACA CTGTAAGTAC CACAACAGAT GGAACTTCT
 CTGTTTGTGTT ATTAGT
 A/G
 TATCCTCACA ATATTTGTTA AATGAGTGAG AGACTCAGGA TACAAAGGTG GAATAAAAGC
 AG

01T205 107bp
 AGTGGCTTTT AAGATTCTCT TTTTGTCTTT GGATTTCAAC AGTTTAATT
 C/T
 TGATGTGTAT AGGTGTTAAT CTCTTTTGAG TTTATTACTA ATTGCAGTCT ATCTGGC

01T206 121bp
 AGATGCTGAC CACAAGCCTA AAACATGAC CCATGCTTCT GGTAAACAG CTAAAAATTG
 GGGTTCCC
 A/G
 TGGCCCCTTC CTCAGTTTTG ATTAATTTGC AAGAGTGGCT CAACAGAGCT CA

01T207 124bp
 TGGCTTATTT TTTGCATAA CAAATTAGAA AGCAATTCAT AAACACAAA AGATCTGAGA
 AGATCTGTTA TTTCTA
 A/G

Table III

AGATTAATAT AGTCCGTGTG ATCAGAGGAA TGTCATTGCT CAGCAGT

01T208 120bp
AATCGGAGAG CAGATTCTAG TAGTTTAGCA GAAAGCAAAA TAGAACAGTT AATAATCATT
AACTTAGACT GC
C/T
GAAGGCACCT GAACTTAGAG TAAAGCATGA AGTGCTTGTC TTTGCCA

01T209 127bp
AAGATAATAG CATGATGCTG CTATAAATAA ATGTATAGAT TGATATCTTA AGTGTTCTGG
TGCTGAGTTA CTCA
A/G
AGAGAAACAG ATCTCTAAGT TTCTGGTGAT GAGTCACCAC GTGAGAGAAA TT

01T211 100bp
GTTAAATGA GCTCAAGATG TGTAGACGTA TTATGTTTTT TTAGGCTA
C/T
TGTTTTTTTT CAACATTTAG CAAATGAATA GGATAGTACA GGGCTTTTTT A

01T213 137bp
ACGCCAGAGG CATGGAACAT TTTCTCCATC ACAGCTCTCA AAAGGAGTCA ACCCTACAGA
CACGTCAATC TCAGACATCC AGC
C/T
TCTAGAACTG TGAGACAATA CATTTCTGCT GTTTAAGCCG TCAAGTCTGT GGC

01T217 134bp
TTAATGAGAA AATGACCCAA TGATAATGTA TATGTAATTA AGATTTTATT TGCTTCCCTA
TACACC
A/G
TGAGAGTTAA TAAATATAAT CCTCTATGGG CAATTTCTTT AAATCACAAG AATATTGGTC
CCTGAGG

01T220 126bp
AATTTTCTTC ATAACACTGT TCTTCATTAA AAGGTAGCTT TATTTTATAT CTCAGTGATA
AAAAGCCACC AAATCA
A/G
TTCTAGTTTT GTCAACTCTG TTGGTATGAG GAATCTCAAG ATTGAAAAT

01T221 120bp
CCAAAGGAAG TCACATTGTT TTAAGTGTA AGTACAAGTT CAGAGGTAGA GGTTCCAAAT GC
C/T
TAAATTCTTC ATAGATTAGT CTTGCTGAAG TAAAGAATTT GAATAGGGGA CATAGGC

01T222 140bp
CCTCAGGCCC TCACACACTC ACCTTTCATT ATTCTTGCTT TCTTGACCAT TCTTTATTCC
TCATTAAGGC CACC
C/T
CACAAATGAA ACTCACCTT GAGTTAGGTA AAAACGCTCA TAAGCATAAT TTTCATCCCT GTGTT

01T223 103bp
TAGGGCATCT TGACATCTGC TTTAGGCACA CTGAAATGTT CAA
C/T
GGCAAGAGTA TTTAGGACTG AGAACATCTG ACCACTCAGA GCAAATTATT TGAACCTTCT

01T224 141bp
CAAAGCTAAA AGGGGCATCT GAGACAGATT TCCTTTTGTT TTCACTGGCG TGTCAAATGC CAC
G/A

Table III

GTGACAGCAA AGGAATAATC TTCAGTTTGT GTATAATGAG GTCTGAAATT TCCGTCGCCA
CATATTGATC ATGAATC

01T228 132bp
CGCTAAAAAG GGAAAGCCTT CCTTCCTGCC CTAGGACATC CCTGCCAACT T
C/T
AGGGAGGTGG GAACCCAGCT GCGCTCTCTA CAGTATGGGT TACTTTTGTG TCTGGAAGGT
GTCTGACATC CTGAGACCTG

01T230 142bp
TGAATTGTAC CTTTAAAAAT GGTAAAGATA GTAAATTTTA CCATCTTCAC AGTTTCCCGA
GATTGCAAGG CCAGCAGTTA AAGACAAAAA CAA
AACTA
T/C
TTCCAAGTGC CCTACAGTGT GCAGACCTTT CCCTTGTCTT GCCCTGAG

01T231 131bp
TTTTCAGCAG TGATATTCCT TGCTATGTGT CATTCTATTT STATGGAACG GCCAAAAGAG G
T/C
GAAGCCATAG AGACAGAAAG TAGATTTGTG GTTGCCAGGG GCTGTGGGGA GGGGCCTGGG
GAGAGATTG

01T232 142bp
ACCATGAAAA TAGATGACAG AGTAGGCACA GGAAGACCAG TTAGGCCCCAT ACAGCAATCA
AGGTAAGAGA TGATAGTGGC CTGGAACA
A/G
CACGTAGCCA TATAGGTGAC TATATTTATA TTTTGAGGGT GATCCAAAAG GAT

01T233 113bp
GGAGGTTGGA GGGCAGGGGC AGATAGGCCC TACCTTTCCA TAGGGTGAGT GGCAAAGAAT TTG
T/C
AGCTATCTTT CACAACAGCT TGGTTAAGCA AAATTTTTTT TTACCATT

01T234 130bp
GGCTATGCTA CAGTCTCTAG CTAAATGGAA GACACATTCA TCCTTCTCC
C/T
TCTGACTGCT TTGATCATCA TTTATTGCAT CTCATAACTA ATTTTCTAAA GTTTGGATTG
GGACTTTTCA GGTCTTTTTT

01T236 128bp
TTCTCTGGGG GAACCTGTCT CAGTGTTGAC TGCATTGTTG TAGTCTTC
C/T
CAAAGTTTGC CCTATTTTTTA AATTCATTAT TTTTGTGACA GTAATTTTGG TACTTGGAAG
AGTTCAGATG CCCATCTTC

01T237 141bp
AAAAGGCTAT GGAGGTCCAA CAAAGAACAT CCCAGCTCAG CAAAATGAGT GGCAGCTTCA
GGTGCGAAGT GGCTCTGATC TAGGCGTTGA GGC
C/T
GAGTGGGATT TGGAAGTGTG GAAGTTGTGG GGAGGAGGCA TATTGCA

01T240 121bp
GGCTGAAAGG ATGAGTGATT TTAAGGGGAA GATTTCTCTA TACTAGCTAG AACCTCTC
G/A
TCACGTCTGG CCCCTGTGAG CCTCTGAATG TGTGCTCCCT GGCTGAGCAG CTGATACACC
CA

01T241 107bp

Table III

TGCTCTTATG TGCCTTTTTTC ACCTCAACAT GCAATGGGAT AATTAAA
 A/G
 AGGGTAGATT TTTTTTTATG AAATAGCATT TTAGATGAGG TAATAGAGGA ATACAGATG

 01T242 141bp
 ATTTGATCCA TTCATTGCTA AAGCAGTAAT TTTGAACCAT ACCATTGCTA AGTACTTAGT
 CATCAATATA GGGTTGAATA GTTCATCTGA CA
 T/C
 TTTTGTTTTA ATTACTAAAA TGTTTTTTTG CCCAGTTCAA TTGGACCA

 01T244 119bp
 TGGAAGGGAC TGTCCTCCCT GCCTGCAGAA TCTGCTGTGG TATCTCTTG
 A/G
 ATGAGGCCAT GCAGCCCCCA CCTGGCTCCA CGTTCATTCT TGTCCTGATC CTCAAGCACT
 CAGGGCCTC

 01T246 99bp
 CTTCCCTTCC CCATTTAGGA CTCTGACGCA GTACAGTTAA TCTGTGCA
 C/T
 AGGAAAGAAG AGCTGTTTGA AGAGGTTATT CGGTAAATGC AGAGAATGTC

 01T247 143bp
 AAAGAAATGA AAATGAAAA ACAGTAAATG AGGGAAAGG AAAATAATGA TGGCAAGGTA
 AGGAGGAG
 C/T
 TAGAAGGTTA TGCAAACTA GAGTTATGCA AAAGTAGGAG CTAGAAGGTT ATGCTAGAGG
 TTATGCAAAA CTCA

 01T248 120bp
 GTTCGTGGAA GCTCACTGGT AGGTGAAGAT GCTTTCTGAG TGATAACATA TGAGCTATTG
 CAAACATGGT
 C/T
 GGGGATTCCA CATGCCATTT AGCAATAACT TGGGGATAAT GTGGTACGT

 01T249 149bp
 TGGCTCTACT TTCAAAAGTT CTTAATTTTA ATATAGTCAA AACTATTTTT TCTTTGGTGG TAAAT
 A/G
 CTTTTCATGT CTTTAAAAA ATCTTCCCTT TCTCTAAGGT TTGAAGGATA CTAGCTTAAC
 TTCTTCCACA GGTTTCAGAA TTT

 01T250 136bp
 ATACCATTCT ATCAAAGAAC GGCATTTGCT TTTTGTTACA CAAATTATTT CA
 A/G
 TGTTTAAGGA CAAAATGAAA CAAAACAGGA AAACCAAATT AACAAGAAAA AATTCCTCT
 ACAACCTTAC CCCTGCCCCG CCC

 01T251 109bp
 AAAGTGATTG TCAATATGGC AAAAAAGTTG GAGAGTGAAG TGTTTCAGTA TATGGATCTT G
 G/A
 AGAAATTCAA GAGCTAATAG AACTACGCA GGAGACAACT TGCTGGA

 01T253 141bp
 TCTCCAGAA TTCCCAACAA CCCAAGGTTG CATTAAATTAC TTTTAATGGC AAAACCACTG
 TTACTTTTGC ACCAA
 C/T
 CTAATATTAA CCTATTGTGG GAGGGACCCA TGGGGAGGTA ATTGAATCAT GGGGCCAGTC
 TTTCC

Table III

01T255 139bp
 TCCTAAACTG AGTGTATGCA GTAGGTGGTC AACAATATTC ATTAGTA
 A/G
 ATTCTTTGTA TTCTTCCTGA GGGCAAACT GCTAAACTC CCTGGAGAAA AAGGCAATAC
 CTGGCAAACA TAAGGCATCT CTCCAGGCTT A

01T256 139bp
 CTTTGTGTTA ATGGCTGAAC AACTGTACAT ATCTGTAAAA CTCATTAAAG TATATATTTA
 AAATGGGTGA ATTTTAATGT AGGTAAATTG TACCTCA
 A/G
 TAAAGATGAA TTTTTTTTTT AGCTGAGCGG GTGCAGAAAC AGTAAGGAAT T

01T257 114bp
 CTACTGTAGC AGAAAGCCAA TAGAAAATGT CTAAATTTTA TCACTAGGAA GCAGCAATAT
 A/G
 AGCATATTAT TTAGGAATAT AATAAGACAT CTCGAAGAGT TGACAGTGGT TGT

01T258 115bp
 CACTAAGAGG TAAGGCAGCT CAAAGGGCGT TGGCTAATGA AGTGGATTAT TGGGAGGG
 A/G
 TTTACTCTTA CGGGTTTTAG TGGGGGAATA CATTAGGTAA GATGTCTGCT GGGAAAT

01T259 137bp
 TCAACTTGGT GACTTATATA TGGAGAATTT CAAATATGTT CTAAGTGTTT GCCTATATAT
 TTTTGGTCTG ACATGGGGA
 A/G
 AGAAGGTTTC TAGGGGAGAC TAATCTCTGA GCACTTACCA GGAGAGGACA CCTAAGG

01T262 139bp
 AGAGGCACTT TCCACCTGGT TACCAACCAG AGTGGTAAGT GGCCATTGAA C
 A/G
 CTTTGGATAA CTTATTAATG GATGTATATG TGTTATTCTG CCTCTTCAAA ACCAGAGGAG
 GGCTATGCTG TAATGGGCTT AGATCTA

01T266 149bp
 GCCCTGAGAC TGTCTGCTAA TTTGGATTCT AGAACAACAC AATCCACCTT ACAAGTA
 C/T
 GTAAGGAGGA AAGTAAATAA CAAACGGGTA AAGTGCTTTG TAAACTGTCT ATACAAATAT
 AAGAGACCGT TATTACAACA CAGCGGAAGA A

01T267 97bp
 TAGAACACAC TGCCCGCAAT ACCCCCCCTT TCTTGCTGCG CCCTGC
 A/G
 GCTCCCGCGT GGAACCTCAT TCTTCCATTT GCCCCCGCC CCCAGTTGCT

01T268 108bp
 CTTGTGGTGA TGGATATCCT AAATACCCTG ACTTGATCAC TGCACATTCT ATGCATGTAA CAAA
 T/C
 ACTCACAGGT ATCCCATAAA TATGTACAAA CTTTATCAAT AAAACATTTT TTAAAAAGAT
 GTGCTTCTGA TCA

01T270 132bp
 GGGGACTGTG CCTTGACAC CGGCCGCGAC CTAGCCCTCT GCCCCCACT CAGTACTTCC
 ATTTAGTCCC GTGGAA
 C/T
 AGGAGAGACC TGTTCCCAAT CTGGCCGAGA AACTAGGGAT GGGGGGACTG TATTG

01T271 149bp
ATTGAAGAAG AAAAAAGAAC AAAGTATTTT TTCCCATGT TTTCTGGTG TCTTTTCAA
AGGTTTGTGT CTTAACAGGT GCCAAGAGCC TGCAATC
C/T
TTCCCAAACA GCCCTTTGTT CTGTGCTCAA GTCAACCCAC TGGGACTTTA C
01T272 124bp
CTGACTCCTT TCCCTCAACA TGCAAGCATG ATCAAGCCTT TCCCATTTTA AAGTAAT
C/T
TTCCAACCTTA CCTCTCCTTT CATCATCCTC TCTCTTTGGC CTTACCATCT TAGCGAAATT
TATTGA

01T273 149bp
CCCAGAAACC TTAAATATAG ACAGACTTTA TTAATTTATG TAGGAAGCCA AAAATAGGAA
ATAAAAAGAT C
C/T
GGAGTTTCTA TATACTGATA TATTCAGCAA CTGAACTTA CAATTCCTTC AATTCAGTCA
GAGCAGAGAC ATTTAAA

01T274 145bp
CAAACCTTGA GGACTCATTC TGAGGCAGAG AATGAATAAA TC
A/G
TTACCTTTGT GAAGCATCAG AATCAGCAGC ACTTTCTGT CCCAGGAGAA GAGGGAAGGG
GAGGATGGCA CGTTTCAGGG CTTAGGGGAG GATAGGGGAG AA

01T277 105bp
CGCAAGCCCA GAAAGACGGC TGGGGGCAGG GGTGCTGCGT ACTGTTCAAT GAGAGCCATA A
T/C
GTGGCTGTAA CTGTCTTCCT CATATTGCAA GAACACTGCT GGC

01T278 124bp
GGTGAATCAG GAAGATTTCT AAAGTCCTAG TTCTACAACT AAAGCATTAG ACGATTAAAG AAG
C/T
CCTTGATATT CTCTCAGAAC TTTCACTGAC CTTCTGCCTC CTACAGACTT CGAGGAAGAG

01T279 142bp
GCTTGCTGT GCTGCTCCCT CTGCCCCACTA GAGGGAAGCC CAACCTCAGG CTGAGGCCTA
GAAGGGGA
C/T
GGCTGCGCCA TGTGGGGCAG GGACAAGGAG GGGAGGAGAT GGCCTGCCAC TTCCAGACCC
CAGTGCGAAA ACC

01T281 149bp
ACCATCAGAT CTCATGAGAC TCATTACTAT TACAAGAAAA ACATGGAGGA AACTGCCTCT
ATGATTCAAT TACCTCCACC TGGTCC
C/T
ACCCTTGACA CACAGGGATT ACGGGGATTA CAATTCAAGA TAGATTTTGA GTAGGGACAC
AG

01T282 145bp
AGGACTGCCA TTTTCTAATT CAGCAAGAAG TCAAGAAGTA TAGGATAGGT GTGAAGGATG G
C/T
GAGATCTGTA AATGTGTAAG CTTCATAACT TCTCTGTGAC TTGCTTAGCT TTATTCTGTT
TTTTTTTTTG TTGGCAAAC GTA

01T283 137bp

Table III

AGCCGGTTGG TCTGGGCAGG AACGAAGTCT GTGTGGTCAA AGGGGACCCG CGCCGGCGAG
 ACTGGGATGC TG
 C/T
 TTGGGCTGGG CGGTCAGAGT ATGGAGTGGG GCTGGGGTGA GGTGGCAAGC ACCCCAGGGT
 GGGG

01T285 149bp
 GTAGAACCAT GAACCAATTA AACCTTTTTT AAAATAAATT ACCCAGGTAT TTCTTTATAG
 CAGTGCAAGA ACAGACTACT AATACACCTA GAGACCCA
 C/T
 GGGACACCAT CAAGCAGACC AATAGATACA TAATGACGTT CTAGAAGGAG

01T286 110bp
 GGTTTTATGC ATTTCCCTCAA AACACCGACT GCTCTTCACG CACTTTCAAA CCATATT
 T/C
 CCTGTTCTCG CAATCCACTA TAGTGATCTG ATACATTAGA AAGCTGCCCT AG

01T287 122bp
 GGTACCAGA GTTCCAATTC AATTAACACA ACTAACTGAC TATTGTAACT TGTAGACATT
 ACCAATGGGA ATTAAC
 A/G
 CTTCTGAAAA AGGTTTATTT CTTCTCTTGA AGAAGAGATT GGGAGGAAAG GTATA

01T288 121bp
 GTTGAGCATT TCAAGATCTT TCTCAGTAAT AAAATAAGTA AAGTATTTTA AAAATAGAAG TT
 C/T
 TCAATAATCA ACAATTGAT CTCGTTGATA TCTATAGAAT GCTCTAATTA ACGGAGAA

01T290 125bp
 GTATGCTCAT TAAACATTA TTCGTTATAG AAAAAAGTC TCATAAAATC TGGAAGCAAA
 TGAATGTCA
 A/G
 TTAAGAGATT ATTTTATCG AATGGAAATA TGAATCAGCT TAAATTGTGC ATTC

01T291 146bp
 CCCAATCTAA ATGTACATCA ACTGGTAAAT GAATAAAAAC ATGTAGTACA TCTATACAAT
 GGAATATTAT TCAGCAATA
 A/G
 TAAGGAATGA AACACAGATA CAAGCTTGCA CTTTTATAAA CCTCGAACAT TATGTTGCAT
 GAAGAA

01T292 121bp
 ACTATTCTGT TCTAAGGTTG CACTCCAGGT TGAAATTGGC TGACAAGGT
 T/C
 TTAGCTTGGG TAGGATTTAT TCCCATATA TTAAATTATT TTTTAAATTA GTTCAATGCC
 CAGGTCATTT C

01T295 116bp
 CTATGTCTGT CCCTTGCCCA TTTACCCGCT ATATTCTGTC TATATTTTC
 A/G
 CTGAATTTGG GTCCTGCTTC TTATGCTTTA TGACAATGTG TGGTACAGCC CTTTGAATCA
 CTGTTT

01T296 143bp
 ACCTGAAAGA AAGGAAATCA GTATATGGAA GGAATACCTG CACTCCCATG TTCATTGCAG
 CACTATTCAC AATAGTCAAG ATACAGAATC A
 A/G

CCGAAGTGCC CATCAGTGGG TGAATGCATA AAGAAATATG GTACATGTGC A

01T298 117bp
 TTTCTGGTTG CAGCACTAAA AGTCAACTTG CCTTTTGTG GCCTGC
 A/G
 TTGACCATT TCTTCACCAA CTAAACACTT TCAACAGAAT AGATAAACTT GAATCCTAGA
 TGAGATAGCA

01T299 142bp
 ACATAATACA GCTGCCACAG CCCTATGTCA TTAAGCAGTT GAATTAATCA ACCACTTTGC
 TACCCACCTC TGAACTTTTT GCTTTTGGAG ATAA
 C/T
 CCCCTTTTTG TTTAACCTAT TTTGTGTTGA ATCCTTACTT ACTCAA

01T300 124bp
 TCAGTGACCC ACAATCCATT CCTAAAAGGG AGAGCCTCCT GTCTTTCTCT CAGTTCCCTC A
 A/G
 GCTCTTAGCA GGACTCAATA AGAGCCCCAG AAATTTCCCA GAAGTAGGTG ATTTAAAAAC
 AC

01T301 124bp
 TAGAGTAAAT GTGGTCTGCA CAGGTGTAGG AAAGAGTGTG GGAGAGGAGG AGGGGACAA
 C/T
 CTCATGCCTT TCTTTATTAA AAACACATAA AATAAACCTT ATAAATGAA AAAGTTCCAT
 GGAT

01T302 103bp
 GGAGCATTTT TTGGTATCTT TATTTTTTAG ACCACATCCT TCATGGTTGC AT
 G/A
 TTGTTCTATT TTCTTAGGAA TGCCTGAAG CTTGGCTTTG CTTTTATGTT

01T303 90bp
 AGGATGCAAC AGGAGCGGGG TTGCCTGATA AGACAGCGAT AGAAAACC
 A/G
 AGAGATAAAG GAAGTCTGGC CAGCAGCAGC TAGTCTAGAG G

01T305 106bp
 GAAGGGTGTG TGCAAGTGTA GAACAAATTC CTTCCGTGAT TAGTCAAGCT ACCTGACTT
 T/C
 AAACAAGTTT TATTTTTGTC TCTATTACTG TTAAACTGCA TGGCCT

01T306 115bp
 AGGCTGAAAT GGTGTCATGT GATTCCAGAG GCCAAAAGGC TGGTGTGGAG TCA
 C/T
 GGCAACTTTC CTACCACTAC ATTCCCCCTT CCTATGAGTT TCATCGTACC AATGATGGCT
 G

01T307 115bp
 ACAACTGTGA ATTGTGGCCA AGTCTCCCAA ACTGGTTTTG TTCAGTTCTG AACTTGCAA
 C/T
 ACACCAGAAA TTTTAGGGTT TGGAAATTAG GAGATCAAGA GTTTGAATGA AGAA

01T308 115bp
 CAGACCAAAA TACATTTATG ACACCTGTGA AAGTAGAGGA AGAAGAAAGG TTTGTGTAGG
 AAGAGTCTCA GA
 C/T
 CAAAATCAC TTCTATGAAA GTTTCAGCCA GGGCCAATGG TG

Table III

01T309 131bp
 AAGAAGCCTC CAGGAAAACA CATCGCTTGC TCCAGGAGTG TGTTCACAGA GTGTCGACAC
 AGCTCCAGC
 A/G
 TTTCTCACAG CCTCTGCTGC CAGGAAAGGA TAAAACACCA CCCATATTCA GGAACAAAGA
 C

01T310 135bp
 GCCCACCCTA ATGACCTCAT CTTAACTTGA TAATCTGAAA GCACCCTATT TCCAAATAAG
 GTGACATTCA
 G/A
 AGGGTGTTAG GACTTCAATA TCTTTTGAGG GGACACAGTT CAACCCATAA CACCTACCAA
 CGGT

01T312 145bp
 GACACTCTGT TGAGATGGGG GTTAGACATC TAGGTACTGT TCCTGTTTCTAT CTA
 A/G
 ACTAGCTACA CAATTGTGAG CACATTGCTT CTTTATCTGT TTCTCTAAGT CCTTCTTCAT
 CAAAATAATT TGAATTTCCA TTTTGCTGG

01T313 134bp
 CAAAAGAAGG AACAGGGAAT ATACCTAGAC TTTAACCTTG TT
 A/G
 ATACTATAGT ACCTGTCCTG AGTAGTACAT TGTAGAGGCC AGCCTGACTA ACTGGAAGTC
 AAAGGAGAAA TACCAAGAAG AGGAATGGCC T

01T314 110bp
 AGGGGAGAGT TTCTTTTTAA GTTATTATTT CATATTTTCAT GGATTTTCATG TCTTCCTCTG
 TCATTT
 C/T
 CTCCAAGCTC AGTTTGGGGA ACCAGCAGTC TGTGTTAGTT CAC

01T316 143bp
 ATCAGGCTCT ATTAATGGT GGTAGGATAT GAGGCTACAG ATAACAGCAA AAAAATTAAT
 CAAAGTTTCA ATTA
 A/G
 CACAGTACAC ACAGATCAAC CCACCAGCTA TTATGTATTA GTTTTAAGCA CTTGTCATTA
 TGCCTCAT

01T317 146bp
 TGGAATACAC AAATTTTGGA AATAAAAGGT TCAAGTTCCA ACATGCCAAA ATT
 C/T
 TACTGAAAGT AACAACTATA TTAAAGCTTG TAGTGACCAG GTACAGTAGC TCATGCCTGT
 AATCCCAGCA CTTTGGGAGG CTGAGGCGGA TA

01T319 136bp
 GTTTACAAAT GAACTCCTTT TCTGTCTTTG CATTTTAGAG AACTAAGTG ACTAAGGAGG
 AATGTCAAGG ATCATAGTGA CAA
 C/T
 ATGTTCTTCA AACGAAGCTA GGAGACTGAG AGGGAAGTGA TGGAGGGCTG AC

01T320 145bp
 TTTGGCTCCT CTATGGGCAC AGCTGGCTCA GAGGGCTCTG AGCAGCATCT TTCTATTCTG
 GGAAACTACA GCCAC
 G/A
 CGCCCGTGTG AGCAAGTTTG CACCATCACG CTCTGAGACC AGAGTCCTGC CCTTTCTCCT
 CCTCTGTGC

Table III

01T321 133bp
 GCACTTGTTA GAAACACGAA ACTCGTGGGC CTGACTTCAG ACCTACTGAA TCAGAAATAC
 TGGATGGGGC TCAGCAATTT G
 T/C
 TTTTAACAAG CTCTTAGCTG ATTCAGATGA ATGCAAATGA CTCTTAACCA C

01T322 141bp
 TCTTTTGATC AAAGCAATTT TTAGTTAGAA GGAAACAGCT GACTTACAAA GAAATTGCAC TGAG
 A/G
 CTATTTCTAA ATAAAAGTGT TTTTGCTGTG GCATTGCAGG GAATTGAGGC ACCTTCCATA
 CTGGTGGTTA CTTACA

01T323 118bp
 AGTTTTCTAC AGAAATCACT CAATGAGCAT TGATGGCCTG AAATGAATTT
 C/T
 GGCTTAAATG GTACAAATGT TCAGAAGCAG GAAAGCTCAG GGCAGGTTTG AGGAAATTAA
 GCAGTCC

01T324 129bp
 CAGTTGAAGC CACTACAACA TCTAATACAT CAGCCTTGGA AGCCATCTTG CAGATCATCT CATC
 A/G
 TGGGAAAACA CACAATATCG ATGAAGCAAG CGATAATGCT CCACACACTG TCGGCCTAAT
 GGCA

01T326 133bp
 GCATAACCCC AAAGGGTATT CTTAGGATTT GTAGGTAAGG GTTTGAGAAG
 A/G
 AATATGTCGG CTAAATATG GAGAGAACT TTTAAATGCA GTCAATAGAT ATGATGGACT
 GCATTAAAT ATGTTGAATT CC

01T327 132bp
 TGTGCTTTGG TTTCTTCTCA GACTGAAAGC TGGACTAGGG AGACAAGTGC TAGAAAATGA A
 A/G
 CATAAAGCAT GAAGGGTATT TTTTTTCTCC GTTAAAGAA CATTACACG GTCCCTAGTG
 TCTACAAAAG

01T328 146bp
 GTGTGTCTCT GACCTGGGCT CTGATAATAG GACCCAAAAT CCCATCTTCT TTC
 A/G
 TATTGGGATT CACTGTATGT TTGGTGAAGG ACTCATCTTC GTACTGTGTG TACATAACTT
 TCTTATAATG TTTTCCAATT TGGTTTGAGA AA

01T330 111bp
 AGTGACAACT TAGACATTTG GTGAAAACCTC ATTTTCATTT TATATG
 A/G
 TAGCAGCAGG TTGTGCAGGA CATGAAGGCT ATACAGTTTT GTGAGGCCTC CTTAAGTAAA
 AAGT

01T331 136bp
 ACCACTCACT CTTTGGGTCC GTGCCATCTT TAAGAGCTGT AACACTCACC GC
 A/G
 AAGGTCCATG GTTCCATTCT TAAAGTCAGT GAGACCACTA ACCCACTGGC AGGAACGAAC
 TCCAGACACA AGATGATGGA AGC

01T335 139bp

Table III

CAGCTTCCAG AGACAGGCTT TTGATCACCA CAGGGTCCTT CCCTTTGTCC CAGTTATCCC
 AGGGAAAGCT ACTAATCTGG TTCAGGTGG
 A/G
 CGTGGGCAGG GGCTGCTAGG CCTGCAAGAA GCAAGCCCAG GACAATCAG

01T336 134bp
 AAGTTGAATT TAACAAGCCT TCTATTAGAC TTGAATGCCT GCATTATGAT AATTATAAGC
 ACACCTTTCA CCAGT
 G/A
 TAATATTTTT CCTCTTAGGA GCTGTATGGC AAAAAGAAGT TTTGTGAAAT TTTATTGC

01T340 127bp
 CCATTCTAAC TGGTGTGAGG TGGTATCTCA TTGTGGTTTT GATTTGCATT TCTCTGATGG
 CCAGTGATGA TGAGCATTT
 T/C
 TTCATGTGTT TTTTGGCTGC ATAAATGTCT TCTTTTGAGA AGTGTCT

01T341 108bp
 GAAGCTGAGG GAGCCCTGGG GCGGTGGGAA ACAGCGCTGA CAGTTAGAC
 C/T
 GTAAGAGCCC AGGGTAGGAA CTGGGCCCTT CGCTCAGTAC CTTGGGCCAG GTCTGGCA

01T342 149bp
 TTGGAGGTAT CATCTTGACT TCTCTTCTGG TCATGGCTTG TTACAGATTT GGCACCTTTC
 ACTTGAC
 C/T
 TGAAAGGAAA CAGATTTTAA AATTACATTT AATTAGTTTG CAATATGAAA CAAAATGAAG
 CCAGTTTTTA AGACAATAAG A

01T343 109bp
 AGTTTCAGAG TTCAGCTTCA AAGCTAAATG TAATCCCCCG TCTC
 C/T
 CCTTCCCCTA CAATAGTAAA ATGAAGAAAG CTATTTATTT CCAA

01T344 113bp
 TTTTGAAACA TGCAGCGCAA AAACCTCAAAT TTCATAGATT GACTTTGTTC TTAACAGAAA
 ATCTCT
 A/G
 TGAAAGGAAA TTTGTGAAGT AGCAAGAGAA AAAGAAAAGC ATGGTG

01T346 132bp
 ATTAACATGG AAGGGGAAAT ATGATAGATA TATAAGGACC CTCCTCCCTC A
 T/C
 TTATATTCTA TTAAATCCTA TCCTCAACTC TTGCCCTGCT CTCCGCTCCA CCCCCTGCCA
 ACTACTCAGT CCCACCCAAC

01T349 126bp
 GTGATCCTTT CAAAAATGGA TTCAGAAATC ATGTCACTGC TCTGCCCAA GTTCCC
 A/G
 AATGACTTCC CAGTCACTCA GAGCACAAGC TGACGCTCGA CACATCTGGG CCCCCTAAGA
 TTTTCATTT

01T351
 ATTCCAAAGTTTTAAATTTTCCCATTCGTGTCATAGTTTGGGTACCCTACTCCTCAGACC
 CGGGGCGAGCCTTCGGCTGTGACTCAGCACATAAAAAACCAGAACGCCGGAAGTATTTTC
 CTACACCCGCCGGATG

A/G

ACGCTGCTCCCGAGCGCCGCAAATACTAATTGGCTCTTCTCTACCCTACAGTCGGCCCGA
CAGTGGTGGGGTTTCATCCTCAAGCCCTAAGAAAGTGCTAAAAAGACCAGTCTGGATGTG

01T353 110bp

AAATTGTCTT GGAGAAGCCC TCAGAAGAAT AGGGATAGTC TGTTTGAGCG TGTTGTCAAC C
C/T
TCAGTCCTCT CTTGTGATCC TAGTTAACCT TCCCTGGTTG ATAAGATTC

01T354 102bp

CTCTCCTCAG GCCTGACTGG CTATGTATTT TCATAAGTGA AGAATTT
C/T
CTGGTGAATT CATGCGATGC GTTCATCAGA GAATAAGAAA CGCAAACCAT ACTG

01T355 142bp

AGGTCTCATC TTCTTCATGG ATACAGTAAT GCTAATAGAA CCCTCCTATT CCATAGTGT
C/T
GGCTGCTGTG AAGGAGAAAG GCAATACATG GGCTACATAT TACATAATAC TATGTAAGTA
TTAGCCTTAT CATTATGGGG GC

01T359 113bp

TGTAGGTCAC TCTATCTCTT CAAATACCCT TTAGTGGTAT TTAAGGTTTT TGCAG
A/G
GTCTGGGGAC TTAGGTGTTT CAACTATCAC CATGGATTTC CAGATTTTGT AAAAGGT

01T361 123bp

GAACAGATGG TAGCCTGTGG TGAAGGTCT CTTTCAGATC TTTAGTCTCT TTTCC
C/T
GTGAATTAAT CTTACCTAGA TCTGGCCAAG AGGAGCCTCA GAGTAAGCCT ATTTGCATCT
GTTATTT

01T362 117bp

TTTCATTAC TTTCTCTGTG CTTAACAAGG CAAAGGGATT ACTGTGCT
G/A
GGGTTACTGC TATACCAAAC TGTCATCTCA GTTCTTCTTG GATACAGTCA GTTTAATTAT
GCCTGGTT

01T363 141bp

AAAACATTCT GCCAGTTATG GTCAGGGAAC TGCATATTTT TAGCTTATCT TCTTCATTGT AAA
C/T
TCTCTAACAC CTAGAACTCT ACCTACCCAT AGTGGACACT CAAAAATAAT TTGCTGAATG
AATAGTAAAT GTGGACA

01T364 135bp

GCGCAGGGAA TACACAAGGC TTAATCCACT AACAGAATAG GTTGAAAATA C
T/C
GAGATTCACC CTCCACCCCA ACAATGCAAG GAGACTCAA GAAATTAATG ATCACAGGCT
GGGTTTGTGA TGAAAGGAAA ACAA

01T366 129bp

GCTGCAGGGC TCTGCTGCTG GTCACCCACG CTGCAAAACC CAAACCT
C/T
CCTCTACTGG GCCCTCAGTT TGCGCACATA AGGAAACCCA TTGCCTTCCT TTAATCAGAC
TAGGGCTCTA ACCTAGTGAA C

01T367 147bp

GAAC TTGGAA ATTGATTTGC ATCTAGTAGC AGACAGGGGC TCCCAACCTG AGCACAAC
A/G

Table III

TACCAGGGGA ACTGTGGCAA GAGGCTGTTC TCACAGTCTC TTCCTTGGC TGAGGGATAG
GCCTAAAAAG ATGGAGTAAA CGACTCCA

01T371 122bp
TCATATATGC ACATTGCATC CTAACCACAC CAGACTTTCA AGAGCCTTTG CCTTTGTTTT
TCAGAT
C/T
TTAAACTAAA TCTTATCTAA CACCACCCCA TCCAGGACCA TTTTGTTTTG TTTTT

01T372 114bp
AAAATGTCTG TAAATTACAG CATCTATAGA CAGCTATGTT TGCAACATCC CTTTAACCAC
G/A
CTATGATATT TGCTAACCAT GCTAGTGCTA TTTGTTCTTA TTACAGACCC AGA

01T373 125bp
TGTAACATCT AATTTGTGGC ATTGAGTAAA GTTTAAGACT TGTCAGACCT GCCTTGG
A/G
AGGGATAGCT TCCCCACCCC TTCCCCAGCC ACAAATGGAA TACTGCATTC CACAGTGAGA
ATGTGGC

01T375 104bp
CTCCTCCATC CACTTAAGGT AATCACAGCA CTGTAAGGGG CTATATCAAA ATTC
G/A
GCATCAGCAA CATAAATTG GTTGACAACT GAGCTGAATA GAGGACCTA

01T376 128bp
GCCATAGACC TCTGCAAGCA AAGCGACCCC AAGCATTCTT TTCTGCCTGA ATAATTA
C/T
GGTTCAGTTC ATCTGTGATG AGAGATATCA GCCCTGCCAC AGCTAATTAC TATAGGAATT
GGCCTTCAGT

01T377 131bp
CTGAAAAAGG TCTCTCTGGC AACAAAGCAA CAAGGTGGAC ACTGGAATGT GAAGGTGCTA
GAAGAC
C/T
ACAGAAAGTG TATTTAGAAG AATGGCAGCA GCCTGGAAAA GCAAGGATGG GGAATGAACC CAAG

01T380 127bp
CCATGAGGCA GATAAGGGAG TATTTACAGA GGTAGGTTAC ACTGGACCTA CCT
C/T
ACGGGCTTGT TATAAGGTTT GGTAACATTG AGAAGCTACT AGGCATCACT GCACTATATG
CATTCCATAT GCC

01T381 126bp
TGAGAATTCT GGCAAGATTT TATTTGATGA AAGTATTCCA TGGTAGTAGA ATACTATG
C/T
GGCCATAAAA AAGAATGAGA TCGTGTCTTT TGCAGGGGCA CAGATGAAGC TGGAAGCCAT
CATCCTC

01T382 135bp
ATCATCATTC AGCATGGATA TTATCATCGA AATTTAAGAA AAGGTATG
C/T
TATGTATTTT AATGGCCTCT AGTGATTCTC CCAGTCCTAA GATTCTATCA TAATTTTAAG
TAAAGAATAT GCCGCATGCA TAATTT

01T383 113bp
CTAACACTTT CCTCTTCATG GGGATAACCA TATCTGAAGA ATGTTTAC

Table III

A/G
TAACTGCATA ATCGATGCTT CCTGGACCCT CAGCCCAACT TTAGATCTCT GGGGGATGGC
TTTA

01T387 149bp
TGTTGAGGAG ATGGGCACTT AATTGAATGC TTAAAAGGAT ATTTTTCCTA AGCTTTTCTT
GAAGCTTAGT AT
C/T
ACTTCTTAAT CACTGTACTT GACAAGTCAA CCTTTTAATC GGAGCCTGAT AAATCCATAA
CATAAAAAAT TGCATT

01T388 140bp
CTCCAGTAG GACAAGGGAA AGAATAAAAT ATCTTATCTC CCTGTAGTGA GAC
A/G
GCTTTATTAA GATTTGACAG TAGTTATTTA ACAGCAATAA TTGAGTTTTA TGCAAGATTA
TACACGTTCT CCTAATCTGG CATCAA

01T389 149bp
CCAAACCTGC AGAGAACCTA TTGGTCATTA GCGATGAGAA TGAAGTCAAG TGTTTATTAC
TGATTACAT ATAATAAAGG TGACTAACAG GGTG
G/A
CTCATAACCC AACAAATTCTG TCTCCTCAAC CTGGAAGTCT ACGCCTTATC AGAG

01T390 124bp
CCAAGGGTAT TAGTCAGCTC AGGCTGCCAT AGAAAGATAC CATAGGTTGG GTGG
C/T
TTAACAACAG ACTTTTATTT TCTCAATATT CTGGAGGCCA AAAGTCAAAG ATCGATGTGC
TCACAGAGT

01T391 148bp
ACAATCACAA GGTCCACAA TAAGCTGTCT GCAAGCTGAG GAGCAAGGAG AACCAGTCTG
AGGAGCAAGG AGAACTCAGG AA
T/C
TTGGAGTCTG TTGTTTGAGG GCAGGAAGTA CCCGGCATGG GAGAAAGATG TACACCAAGA
GGCTA

01T393 141bp
CCCTATGATG TTCCCTCTCT CCCCTCAATG ACTGTAGCTC TCTAGTTCTC TTTCTACTAC
ACATTCA
C/T
CACTTAATAT TTTGTACTGC TTTCTTAACT GACAATAAAT GCTGGCCAAT GCTTTCCCTG
TTTGTGCACA ATA

01T394 137bp
TTCTTTAAAT CAAGCACAGG GCAACATTGA ATACATTTTC CTACTTTATA TAGCATTTCT
GCAAGTGCTG GGGTTACATT TTAGTCTTCA
C/T
AGAATGCGTG ATTCAAAAGT TTATTTTTTT GATTTAAAGA CACGAA

01T395 117bp
GATTTTGGGA TATGGTGAAA CATAGAGGTC TAGTTTCATT CTTCTGCATA TGAAAATCCA
GTTTTCCCTAG AAC
T/C
GTAAATTGAA GAGACTGTCT TTTCCACAAC ATCCCTTTGT CAA

01T396 133bp
GGCTGAAATT TCACTTCCTC AAAAGAACAT TTTCTTGACC TCTAACA

Table III

C/T
TCTAAATCCC ACCCACTCCC TGCTTCATGT ATCTCTTTTC TGTAGCACTT GCCATAGTGT
AGGTTTACCA TGAATTAGTG TGATT

01T397 145bp
CCCTGATATC AGCTAGGGGT CATATGGATA CTGGCTTGCC C
A/G
TGTGCTAGAA CTGGGCACTG GGATGAAGGA ATTACTTCAA CATGTGTTTG GATAGTTCTA
CCCACCTTTT GCAAGGAGGT TGGTTTGTGC GTCTGCAACG ACC

01T398 149bp
GTCCCCACAC TGGGCTTCTG GACAGGTGGC TGCCAAGATG GGGGGACCCT GCCCC
C/T
GAGGCCTCAC CTTGACGTTG TGCATGCTCA TGAGGTTCCC ACAGTGGTCC AGATACTGCT
TCAGGTCAC GTCTTGAAC ACAGAGCGTG GCT

01T399 144bp
AAGGCTGGGA GGTGCCCCCA TTCTCTGGGT TGGAGCGTGA TGGC
A/G
TCATCTATGG TCGGGGCACA CTGGACGACA AGAACTCTGT GATGGTCTGA GATGCAATGT
TCCCTCTGCC TTGGGGCCCT AAAGATCAAT CAGGATGGG

01T400 147bp
AAGCTCTGAC TTGTCCTTGG CTGCAAAGAC CTGAGGTCTT CTCTTTCTAA GGCTCCTA
A/G
AAAGTGTCTT CTTGCAGCAT CTTGGCCAAT TCTCACTGGA GTTCTATTTG GAACAAGTAC
TAAAATGCAA GCCAGAGTCA ACAGAAGA

01T403 131bp
TAAATAATCC TGCAATAATT CCTGAAAAGT TGTAATCAC TGACA
G/A
TGAGCTTGGG GTGTTATCTC TCTCAGGGAC ATTTGTATTT TAATAGGAGT CTCATAATGC
TACAAAACT TTAATCAAAG CAATT

01T404 137bp
CAGCCACAAA TCTGGTCAAT GAAACACACC CAAGAACCTG TAAGATTATA
T/C
GCCAGGTTCC ATGGGAAGTG CACTTGAC T TCTCTCCCAA GCAGTGAGTA GACTGAAAGT
TTCCAAAGGT GGGGTTTTGT GTTACC

01T406 125bp
AACCACCTGA TGACGTGTGT ATTAAACAAA CAAACATTTT GAAGTGCATT CTTTATAAGG
TAAGGCTTGG GAGGAAAGC
C/T
GCCCACAAAT AACCTAGGAA TTAAAAAGGT AAGCAGAAAC AACTT

01T408 124bp
GCCTCAGTTT TCCCCACTGT ACCATGAGAA TAGTAGCTGT ACCTTTCTCC TAGGGTTGTT
GTGAAAGTTA AAT
A/G
AATTAAGGTG TACATGCTGG TGCCTGACGC ATAAGTGTGC TACATGTGTG

01T410 109bp
CTGGGCACTC CCAATTTCTA GTCATTCAAT ATCTATTTTT CTCCTTCTTT TCTTCA
A/G
ACCTTGTGTC TTTCATTTAG TTTCTCAATT CATACAAAAC CGCATCCAGG AC

Table III

01T411 148bp
 CAAAACCTGC AGGGCCAAA CAAATACAAC GCATCAGAGG CCCCACCTCC TAACCAAGGA
 AAGGGTAAAG GCAAGAATAA CACCAAGAGG CCACCAGCC
 T/C
 CCCATCAGAC GGGCAGGACC ATGGCGGCTC CTAGCACATA AGCCTCGG

01T412 104bp
 TAAAGCATT CCAAACAAAC ACAATTTAGG ACAATTTGTG ACA
 C/T
 ACATTTGCTT TAGCTAAGAG ATGAGGATGA TTCAAATTG AACCATAACA CGAACATATC

01T414 121bp
 GGGAGATGAA GATGACCCTA TGTACATCTT CCAGTCCAAT TATAAGGCA
 C/T
 ATATGGCCAG CCATGTGACC CACATGCCCA TAATCAACCC CAAGGAGAAG TACAAGCACC
 TAGCCATAAA G

01T415 133bp
 TCTGGGGATC TCTTAGGTGG CTGGTGATTC CTCAGAGCAT TTTCCAC
 A/G
 CTTACCAGCT TTTCTATTAA AGAGGTTTCTG ACTGTGCTTT TCTGTGCAGA AATGTTTATG
 TCTTTTTTTT TTGAGACAGG GTCT

01t417 134bp
 GCACACATTT AATTTGTTTG CACCAAAAAA GAACAGTAGA AAACAGTCAT TAATTTAAGG TA
 A/G
 GAATATATCA TCCCTGAATA CAAAAGTAGG TATTTACGGG TCAAATGCAG AATATTCAGT
 GAACAGTTTC C

01T418 132bp
 CCTGTAGGGT CACCTGGAGC TGCAACAGGG AATTTTCTCT CCGTATACCT AACTG
 A/G
 CCAGAGCTTA AAACAATTCC AGATCTCCTG ATCTATTG GCTGGATAACA TAAGAATGCT
 ATTTTGGTGA AGGTGA

01T420 135bp
 CTCCAGAACG GGCAAACATA TAGAGTCAAA GCAGATTGGT GATTTGCTAA
 G/A
 GGCTGCAGGA AAAGAAGATA GGGATATTGG GGATGATGGC TAAGTGGCAT GGGGTTTCTT
 TTTGAGGTAA TGAAAATGTT CTCA

01T421 123bp
 AATTCTTCAA ATCACCTTGT CGAATTGGGT GAATTAAATA GGGTTCTGTC CCTAAACTGT
 GGCTTCAGTC AG
 A/G
 TCTTATCTTC AGTCTTTTAG GTTCCCAAGG TTTGTGCAAG GGCTATCATG

01T424 124bp
 GTCAAAAGAG GTCATTTTGG AACTTTAAGG TTTAATGAGT GCCCTATTAA ATTTT
 G/A
 GATTGTCATA GGACCTGTGG CCCCTTTGTT TTGGCCAATT TCCATTTGGA ATGGGTATAT
 TTACCCAA

01T425 145bp
 GCCTTGGTAA GAAAGGGATG GGAGACAAGG CTAGAATGGT AAACAGGGTT CAGACTACAG CTAC
 C/T
 CAGTGGTGGG TCTAGAAAAA TAATGACCCA CATAGAAAAG TTAAGTAAAC ATATGATCGA

Table III

GGAGTTTTCA TAAAATAACG

01T426 149bp
ATGCGTCTTC CCAAGGATAC GATGCACCCA CCTTCCTTCT GTCC
A/G
GTACCTCACC ACACCCCGTC TTA CTCTGGG GCTTTTCTTT TCCTTGCAACT GAGAACTAC
AGTTCTCTCA ATTTTTATT C AACTTGGGGG TTGTCACCAG TGTT

01T427 131bp
ACTTCCTGCT CATCATCAAA CAGCCCGCCA AATCCAAGTT AAAGGATCTC CATCCCAACA
TCCCTCTAGC TAGATCCTGA ATCCCC
C/T
GTGGCTACCC CTGTCCCATG TAGAGGGAAG TGTA ACTAAG GGAA

01T428 109bp
GGGTATATTC AGAGAGTCAT GGTAAATGTT TCTTGCCACT AAGAGAC
C/T
GAAGACTGTC GTCTGATCTA TGCAAGAGAG AGCTTAATTA GGCATAGACT GGAGTCTGTT
T

01t429 93bp
ACCCACATTC ATTACCCAAC TCTTCATCTG AACCCTGTGG TG TAGACA
T/C
GGGCTAGAAA GGCCAGAATC CAGTCTTTTG GAATGCATGT GGCA

01T430 149bp
TCAGTAGCAA ATATGAAGCT GTTACATACA GATACTGAAT AAAGGTTAAG TAAAATCCTT
CACTCATTCA ACAAATATTT ATT
A/G
CTCTAAGCTT GGTGCTAGTA TATCAGACCT AAAATTTAGA GTGCCACCTT AACATCTTTG
AGCCG

01T431 121bp
TGTCTATTTT TGCTTACGTT GCCTATGATT TTGGTGTCAT ACCTAGGAAA CCATTGCCAA
AAGTAATATT TTTT
A/G
TATAGTTTCA CAACGGAATC CCACATGAGG AACAGAACAA TCAGTA

01T432 115bp
GAGGGGCATG GCCAGGAGAC AATGACAGCC CAGTGTCAGA CGTGCTTTAG TGTACACACT
TAGAAG
G/A
TACCAGAGAT GTGTAGAAGT AGAACTACCT AAATCTGCCT GGAGAAGG

01T433 142bp
TCTGTGCTAG ACATGGTGAT GGGCACTGCC AATTAAATCT GTATTATAGT TTAAAGCCTA
A/G
GAAGAAATTC TCAAATCCAT TTCACCTATC TTAAATCTTA GCAAACCAAC CATACTGTGT
CCGGGATTGG TTCCTTCCGG T

01T435 126bp
CCCCTTTGCT TGAATTCTTA GGCTTTTGTT CTATACTGAG AATCAGCCAG TGCTCCTTAG
GGGATATACC TTGAA
A/G
AATATCAACT CATCTGTCTG AGATTCCTTT GACTTCAGGA TCTTAACTCC
01T436 148bp

Table III

AATGACAATT TCATAGCTTG GGCTTTGATG GGTAACCTGC AGCCCCACTG GCC
G/A

CTCCAGCAGA TGGTGACCTT GTGGGTGGTA GAGAGGCTTG AAGGATCTAG TGCATCTCAG
CTGAAAGTGG CTTGTCTCAA ACAGATGTGA GAAG

01t437 142bp
TCTATCTCAA GGACTGAGTT CTTTCCTGGA AGCATAGCTA GGACTTTTGT TATAGAAGCA
AGTCAAGGAA GAGAAAAATT TTAAAGAG

C/T
AGATAAAGGA AATGGCCCTA GAAAAGTGAC TCCCAGGCC ACATCAAATA CTA

01T438 129bp
CCCTCGGTTG TCAGTTGCTG GTTTTGCACA CTGCGTCAGC TTCTCCC

A/G
TGTGCCTCTC TGGCTGGTGA GCCTTCATTC CCCCTGACT GGCTGCCCTG TCCCTCTCTT
ATTAAAGGAT GCCTTGGGCA C

01T440 145bp
TCTTTTTTGG TCTCCTTTCA TCACTGTGTG ATTTACTTTA ATAGTACCCT GTCAAACCTAG
ATGACTCAGT GGCCTCATCA

C/T
AGCTTACAGA GCATTTTCATC TGTGGTCATT CATCCTGCCT ATGAAGAAAT TGACATGTAG TCAC

01T441 149bp
GGTGGGGTCT TCCTATCTTA GACCCCTGTA TTATATAAAG GTACACAGTG CACCTCTTCA
TAACATTCAG TAGT

A/G
TGACTAATGA CTCACTGAGT CCCTGTTTTT CCCATAGAGT TCCAGGCTCC ATGGAGTTCC
AGGCTTCATG AGGG

01T443 140bp
ACTCAGGGTC CAGCTCTTAT GCTCCTGGAA CAGATTGTTC CAAGGTTGAA TTCAGACCGC
C/T
GCCATTTCTT TGCTCCAGGC TAATCTTAAA TGTTCCACCT GGGACACTGC TTGCTCCAGC
ACCACTCTTT GCTTATACT

01T444 133bp
GTCAAGTTAT GCGGAAAATC CTATTAGAAG TATTTCTTGG TATT
A/G
GACTAGATTT GTAAGTTGAT TGGGTGCAGT TGAAATCTTT AAAAACCCT ATTAAATTTG
TGGATTTAAG CCCAAAAGAC CCTAAATA

01t445 145bp
TCCTACTGAA GTGGCACCGG ATTTTGCTGT TGGGGGAATG CAAAAGGGTC AGGCTTCTTC
ACTCTCTCCA TGAATCAGGG GTGGTAGGAA CAGAGGCAG

C/T
GACTGCTGGG AATTGAACTC ACAGAAGAAA GCTGAATCAT GGCTC

01T446 144bp
GACATTTTAA AGGCAGCAA TTCAAACTA TAACTCAGGA TAGACACTGA AACCATACTT
C/T
GCACCAGATT AAGAAAAGTG GCTGTTGGTA GTTATCAGTG AGATGGCTTC TTTTAGAAAA
TTGTTGGCAA TGAAATAAT ACT

01T448 125bp
ACTTGAAAAA TGTATTTCAA ACCTGCATAT TTCTCTGCAT CTCCACAGCC ACCACGCTAT
TTAAGCC
G/A

Table III

CTGTTATCAT CACCTGGACC ACTGTGGTTT TCTCTGTTCC CTAACGCACC TCTTTTC

01T450

CTTACCAGCA CTTGATATTC TGCGCTCTCT CTCCCATTCC AGCTGTTT

C/T

CTTTCTAACT GCTCTTGTCTG CTCCCTTTC TTGCCTCTCCC GTTCCAGTCT CTCCAGCCTC

01T454 144bp

CTAGACTCAA CTGGCTGGGT CACCGATGGC CATTTCATCT GTGCGTAGCT ATAGGGATTT
AAATAGGAGG ATTTTGTGA AATGAAGACA ATTGACC

A/G

ACTGTGCGTG GAATCAATGT GCAGGATGAT TCACCAGGCT TTCTGC

01T455 147bp

CTCCTGACCT GAGGTGATCC GCTCACCTTG GCCTCCCAA GTGCTGGGAT TACAGGTGTG
AGCCACACCG CACC

C/T

GGCCAATAAT ACATTTTAGT TCAAGATTAG TGAGAGCTAA GGAGAAATGA GAATGCTGAT
TGTTCTGAAA TT

01T459 120bp

ACAAACAGAA GCTACATGAC AAGTTTTGCT CTGTTCAATT TTTCTCTTA AACTCTACTG TGT

A/G

CTGTTTGGA AACGCTATTA TTTCAGAAGG GAGAATCTCA TCTGGAATCA GAAGAT

01T462 149bp

CTGCAAAGTA GATATCTGA ACCCTCATTT TACATTTGTA GAACTGTAG TACAATTAAG
TGATTTACCT TGGACCAC

C/T

TCACTATCAT TTGAATCCAA TTATATCTAG TTGCAAAGCC CACTCTTT CCACTACATC
CTGGTAACTG

01T464 145bp

AGGTTAGAAA AGCAAACAAA GGTACAGTAT ATCTACAACA CCTTAAATTT GCCACTGAAG
TTTAGATTTA CAAGTCAC

G/A

GAGTTTCACT TAATTTCTGC CTGAATATGT GTGAACACTC TTGGGCCATG AATGCCGAAC
AAGGCT

01T465 137bp

TATTTGCAGT GTTTTCTGAC AAATATTTT CCTCCAGATT TTAAGC

A/G

TGTTATGATG AGTCAACCTT TATGTTTGTA AAGCCTTAGT CTTGTTAATA ATGTATAACT
TCCAAATGAA TCATATACTT ATGCATAGCA

01T469 125bp

GCAGCAATTT TAGAACCGTT CTAATTTGAG CCAAGACATT GTCTTCATAT GCCCA

C/T

ATCTGCTAAT CAATGGATTC TGCATGCCGC TGGATGGAGC TATAACCTCC AGCAGGGCAG
CTGCCTTTT

01T470 115bp

ATTTGAAAT CACAAGTGTG GGTATCAAAT ACACATAGGT GCTCTTAACT CAAGGATAAT T

A/G

AAGCATGAGC TCAGGCTCAG AGAGGCTAAG AGATTTGTCC AAGATCACAT AGC

01T471 133bp

Table III

TCTTCTCTCT CTTTAGCGCC TCCCTCTCCC TCTGCTATTG CTTGCCATGT TGGAACTGTC
 AATCACGGGA TCCTCTCCCA CTTTCA
 A/G
 CAAGGGAGGG CAACTGACCC AAGCAAGGCC TCTCAGACTC CTCCTC

01T473 131bp
 TTTTGAACCA CAGGCCTCAT AACTGAAAGT AGACTCACCT TTTTCAATAA TAGATGACAA
 AATGTCGGAA TGTTTGCTTC C
 A/G
 AATATTTTAA TTTGGCATT ATCCTGAATC ACTTAATATC CCTGTGATG

01T474 143bp
 CTGCCACACC TCTGTAGCCC AGAAAGGAAA TTTTCATATT TACTTCTTTA GAGAAACCAA
 CTCCAGTCAT CTACAG
 C/T
 GCTTCTTTTC TTTCTGACCC TTGGAAAAA TGTTATTGTC CACGTTTTAG CTCATACTGC
 TGGCCT

01T475 14 bp
 CTAGAGAGGG CCTGACAACG AAGCTGTTGT GTCAGGGAAA TGAACAAGCA GAATTGTTTT
 TTCATTGGGC
 A/G
 GGTAATGCAT TTATGTTTCT GAGGGAATGG ATACATCTTT CCGTTTATTT TTTAAGCAAG
 TAAAACAAAC AAAACAA

01T477 107bp
 CAGCCAGACC TGCCCTGACT ACAACCCCCA CACTTCTTTC CTGTGTGAGA AAG
 C/T
 AAGCCCTGGT TCTTCCGTT TCTATAGCAA TGTTTTCTGT TACGCGTAGC CAA

01T478 143bp
 GCTGGATGGG ACCAGAAAGT GAATACGCCG AGGCATAGGG TTGTAGCAGA GAAAGAGGTT
 TCATCGTAGG G
 C/T
 CACCGAAGGA GGAAATGGGA GGAAACGTCA AATCCATCTC CCTGAGGAGT TTGGGGCTGG
 GGTTTTTTAAG G

01T479 106bp
 AGAAGGGCGA GGAAGGACTC TTCCCTGGGG CTTTCAGAGG AAGCACAGCA C
 G/A
 GCCGACACCT TGATTTCAGA CTTGCAGTCT CCAGAACTAT GAGAATACAT TTTT

01T481 134bp
 CCTGGGTCCA TGTGGATGGG CCTTGAGTTT GAGTCCATGG GGTTCAGCCT GGTGCT
 A/G
 GGGTGAGCCT GGAGCTTGAG TATGCAGAAA GAGACCTGGT TCTTGGGCCT GTGGGGACCT
 GTCTGGATCT TGGGTCC

01T482 147bp
 GTTTCCAGCA AACTGTGAC TGTACTTTTA CCAGAAGAAA TATATTAGTG TAACAGATGT
 TGAATCTACT GTAGAAGCTG TGTG
 C/T
 TAAACCTAAC ACATGCCTAC CAAGTAAAG TAACTAGTTT TGCTGTTTTG TTTTCTCAGT
 GC

01T485 148bp
 AGTCATGACC TAAATTAAAC AGCATATTCA ACTTAACAAA TTCCTCTATA AACTT

Table III

C/T
TATGGATCCA CTGAAAAATG GCCATCTGTT TCCTTTTATG AAGTCAAATC ACATCTAGAA
AATGGCACAC ATACCGTAAG TGTTCCCTCA TT

17D143 not use Bsl1
CTTCCTAACT CGGGGGGAGA ACGGGGCCAG GCCGCCCAGG GGCA
G/A
GAGCTTTAGA ATCAGGGTGA CCCCCACCCC TACTCCCCAA GCACAGTCAC

17D256 116bp
CTCCCAAATG GATATTCATT CACTGCATTC ATCTTACCTT TTCTGAATGC A
T/C
CACATTTAAA GCCGCACTAT GGGGAGCCAC GGATACATAG TCACTGTCAT TAATCATCGT CACC

17D279 108bp
TAGAGATGGA GTTTCACCGT GTTGCCAGG CTGGTCTTGA ACTCCTGGGC TGAGGTGAT
C/T
TGCCAGCCTC GGCCTCCGCC TCCTTTTTGT CCTTACATCT TTTATCGC

17D350 142bp
GATCTAGCCT CTCTCCAAAC CCTTCTTTTG TTATAGAGTA TAAAATTCTA GAGTGAAAAC TAA
A/G
TTTCATGGCT CTGAAGACAT TTCCCTATTG TGTTTTTATT ATACTGTACT TGAAACTATT
GCCATTGTGT GATACATC

17D402 139bp
ACTCCAGCCC GGGTGACAAA GTGAGACCCT GTCTTAAAAA CAAAAAAAAA AAAAAAAGA
AACTTGTTGG CTCGATTTCA GTGTTCTTCA
A/G
ACTTTGGTTG GTTGACTGCA TGTACTATTG CGAGGGAAAA ACATTCCA

16_001 125
CCTCAGTGCA GCTCCTGGCT TACCCTCTTA CTGTGGGGGA TTTACAGGCT
GGAG
A/G
TTGGGCCGGC ACCTTTCCAG AGCAGTCATC CCTCTGACAT GTTCAGGGAA
TTTGCCAGG TCTGCCATGG

16_002 139
TGCTTTTTGT TTTCCCCAAG TGTGCAGCTG GTGCTGAGAG GTGATGGTGC
TGCTTGTCCT CACACAGGAG GAGGAAGGTG AGGACGGCGA TCCATC
A/G
TCAGGGCCCC CAGGGCCGTG TCACAAGCTG CCTCCCGCCC CC

16_003 106
AGGGTTGGGC AGTGAGACGC GGCTGGACCG CAGCAAAGGA GATGC
A/G
CGGAGCGACA CAGTTCTGCT CGACTCCTCG GCCACACTCA TCACCAATGA
GGGTAGGCTG

16_004 127
GGGCCACTTA GGCGGGCAGA ACGCAGGGGC CAAGGAGCAC CACAGGAAGA
TCCCAGCCCC GCTGGCGATG G
G/A
CACCTGCGTG CAGGCAGAGG GCAGCACATG GAACAGCAAC ACAGGCCTGC A
ACAGG

16_005 145

Table III

GTGCGTGTTG ATGAGTGGGT CGCACCAGGG TGGAGCCTCC TAGAAGGGCA GGA
C/T
GCACCATCCT TGGGGAGTGG CCTGGAGAGG CCTCGGGAAG GGGGTCCAGG
GTGGCTGAGC CTCAGCCATC ACCCCATGCC GTCCAGCCCT

16_006 108
GCACAGCCCA GCAGGGGGTC CTGGGCCTCG TCTGCCAAGC CTGCTGCATG CCTGG
A/G
AGAGGGGTCA GCTCTTGGGA CTCTGGAATC TTGAGAAGGC TGATCCCTGG TG

16_008 147
GGATGGCTGC AAAGTGCAGA CCGTCTGTGC ACGAGGGATG TGAAGAACA
TCTCCCCAA GTTCAGAGCC AGTTCCAG
G/A
GTGCAGGCAC ACCCACGCAG AGCCCTGCCT CCCCTAAGGA GGGGGGAG
GTCAGCAGGG TCCAGGC

16_010 115
TGCGTTAACT TTTTCGAGA CGGGAAACTG GGCAACAGGG AGGCTACAGG
CCTTGCAGGA GGCCATCGGC
A/G
AGTCCGATGC TCAGAGCACA AACGCCTGGCC TAAGAGGTGG TGTC

16_011 118
AGGGTGGAAT TCTCTGTAA GTCCACCCTG CCCCAGGGTG CTCCTACCCT
CTTGGTCTTT TTAAAG
C/T
CAAGGTGCGA TTTGGGCACC TGA CTGTCCA GTTTACCTTA ACAAGTTTGG
GA

16_012 145
GTCTGAGTCT CGAGTATGTG ATTGGCCAGC ATCTTGGGGA CGGTGGTG
A/G
AGGAGAAGCA GATGTCCACA AAAGACAGGT TGCTGAGGAA GAAGTACATG
GGGGTGTGCA GGCAGGAGTC TATGCTTACG GACAGGATGA TGAGCA

16_013 96
CCCTTCTCCT CCCAGCCGGA CCAGACTCTG CGCACCAGG TGTGGGCT
C/T
CCTCTGTGCC GGGGTGTCTC CACTCGACTC TGTGATGTT TGGGATG

16_014 135
ACATTCTGTG GACTTGGACA AATGTATAAT GATGTGCATC ATT
A/G
TAGTGT CATG CAGAGTATTT TCACTGCCCT AAAAGCCGTC TGTGTTTCAC
CTCTTCATCC CTCTCTCCTT CCCAAAACCC TGGCAACCAC T

16_016 149
CATCACCTTC CAGAGCTGGA GGGGACGGCC ACCCATACCA AGGTCCTTTA
GCTGACACCT AAACCTCAGGA GCTAACCATG TG
C/T
AGGTCACACA GGCCGAATCA CAGCAGTGAT GAGACGCTGG GGTCTCCACA
CAGGAACCCA ACTGAC

16_017 123
AAACCCAAGA CAGCTGAAGC GGGCTGTGCG TTTGTCCCCC AGCTAGGCCC
AGGGAGTGGG CATCTGG

Table III

A/G

ACGCAGGATC TCCTGTCCTC CCGACACCTC ATTACCCATA TATGGGCACC
AGCCT

16_018 115
TAATCCAAAC AAACCTAGAGG CTAATTGCCA TTCCCCAGCA CAAAGCTGCA
GTGACGATGA TTCTTTAATT C
C/T
TTCTACGTGC TCACAGCCCCA CGGCGCTCTA CTCTGCTCAC TAA

16_020 117
TACCTGCACC AGCCCATTTCT AGACCTGGCT CTCTTTCCAG GCCAGG
C/T
GGGAGCTCCC GAGAGGGGTC TAGGCATCCC TGAAGTCCAG GCCTGTACTA
TTAAGCAGCT CATCCTGGTT

16_021 132
TCAGAGAAGC CTTATGCCGC TCGATTTCCC ACCAGCTCTG GAGTCGGGTC
CTCTCCACTT CCACACATTC
A/G
TTTCCACAAG ACAGGTCACC TTTCCACCAG TGTGGACGTC TCACAGTAGA
ATCAAGGACA A

16_022 98
GGAAATGCATG TTTCCCCAAA CATGTACTCT CGGAGGTCAT ATTAGTCT
C/T
TTGCTTCCCT GCTCTTTTGT GACAAGCAAT GTTAGGATAG CAGTGGATG

16_023 128
TCTCTCCTTC TGAATTTCTGC GATGGGCCCG GGAATTTGGT TTACATAAGC
AGCCCCGTTT CTCAGACCCT
C/T
TGTATCTTCT TCTGGAGTAT ATGAAGGCTG TGGTACCAGG CCAAATTTTG
CACACAA

16_024 121
AGCCGGGTCC CTTCTCATC AGTCACCATT TAATGGAGAC TGAATGGTTG TGGATAC
C/T
TTTGTTAGGG TCATCAAGAA GGTGTGCCAT GCTTGGCTTG GTAAGGAGGA
GGTTGTGTGC TCC

16_025 89
ATCTTGTCTT CCTGTCACAC CCACCTGGCA CCACCTTCCA CCCAGCT
C/T
TGAGTCAATC CACCACTTCC TCACCTGTCA ACCACCAAGC CTCATTAC

16_026 105
TCTCCACATT AGGGCAAAGT GAGCTCACAT CTCTCTTACC TGCTCTCTGG
GCCTCCC
A/G
GCCTGGACTC GCACAAGGGC ACCATCCCAC TACCCCTCAT ACTTCCA

16_028 92
TGCCCCACGG GCCTTACCTA GTCCCCGAGA ACTTCCGGGA GAG
A/G
AACCTTCAGC TCATCCAGTC CATCAGGGAC TTCCTGCAGA GCGACGAG

Table III

16_031 136
 TCCCTCCTA ATGTGTCAAT GGCTTTGCCA GGAATTGCAT CGGTGGTGTG TCAGG
 C/T
 GGGCTGTTGT CTGGTTTCTG TGACAGAGAC CCTGAGCAAC ACTGGTTTAG
 ACAAGGTAGA ATTTTCTTTC TTCCCACTTG

16_032 149
 TGAGGCAGTT CTGTGAAATC CTCTGCATGG GCTTTTGAAA TTCCAAGGTT
 CTCTTCTTAA GGGCAGG
 C/T
 TGCACAGTAA TTTCCCGAGG AAGGCTTTGT TCCATAAACC CAGGCCTTAC
 AAACAACAGT TTCCGCCTCT GATATGTATA A

16_033 141
 GCATTACTCT AGAATTGGCA TCAACCCCAA GCAAGGGAGC AGGGCTTTCA
 TTCTTATGTG CCTA
 C/T
 GAGTCGAGTC ATTACCAAAA GAGATGGAAA CTTCTAGCTA CTCTGGCTCA
 TTGCATGTTG AGGGAAAATT TCTCCA

16_035 120
 CACGCTCAAC AGCTGTTCCC CTAGCTGTAT CAAGTCCAGG CCAGTGAGCT
 TGCTTCTCTC C
 A/G
 GCTTGTCTCA GCAATTTTGT TTTCCCCAC TGCACAAGTT CCTAACAGCT
 CCAACGAG

16_037 147
 ATGGGCGCAT GGGCTCTTTT ACAAATGTGC CGTGGTCCGT GCATTGTGCT
 GCTGTTGTGC CCCTCTGCTG CAA
 C/T
 GGCAAGGAAG TCCCTTTGCC TTGCGTACAT GGAAGTTGGG TGCCAGGCTC
 CCAAAGCAGT TCTTCTTGTG CCC

16_038 127
 ACTCCCCCAA ATCTGGGTTT GAATCCCAGC TCCACCACTG CAAGTCTGGT
 TGCTCTGGA
 T/C
 CAGTTACTTA ACGTTCTCTA AATGTCAGTT ACATCCGTGA GATAAGCTAC
 CTCGCGGGAC TTCATTC

16_039 111
 TTGCCCCCTCT GGAGTTTACA GTTCGGGGGC AGAGACAATG AATAATGAG
 A/G
 CAGATAAGTA AATAACGGTT TCAGATAATA CTAAGGGCAA TGAAGAAAAT
 AGTACAGGTG A

16_040 143
 CATCTACAGG GTTCCTTCGG GCTATGTTTC TAGGGTGAAT GGCTGAGATA
 TAAGTGATGT GCTAT
 C/T
 CAAGGCCTTT GATCGGTAGT GGGGGAGACT CGGGGCAGGA GATGTTTTTG
 GCGTACCCTG AGACACCATC ACATCAT

16_041
 GGGTTGCCGT TCTAATTAAT CTCTTATCAG TGCAGTCAGG GGTCTCCTTT

Table III

GGAGCCTCTT GTGGGGGTCC CACTTCAGTA GTTACTAGAG CAGCTTT
 C/T
 TGTTACAGAG GTCCCTTTT GAGTAGGTC ATAAGGAATG TGAGAATT

 16_043 124
 CACACTGAGG CAGCACCTCC GGGGAAGTCT CCGTGCTCCG ATGCTGTGGC C
 A/G
 TGTACAGCAT ATGCAGTCCC CAAAGGGATA TTTCAGCACA GAGTTTCAAT
 GTAAAATGAC ACACGCTACT GC

 16_044 135
 GCATAATCCT TAGCACTTGA AGACTTTTTTC AGCACCAAGG ACAGCAAAAC
 GTCATCGTAA TCAGCACCCA
 C/T
 AAGCATCCAC CTTAGGATTG CCTAGGGGCC GGCCGCTCTC ATAAATACAT
 AAAGGGGAGG AAGG

 16_045 138
 AGGGCGGCCT CTCCTGCAGC ACGAGGCCTA CCTGAGGGGC AGTAGGAGGA
 TGAGTTGGGC ATTCTCC
 A/G
 CGAGAAGCTC TTGACCACCA GGCTCTGGCC CCACTGCTTG CGCCGCCACG
 CCGTGCGGCA CTTGGAGTCG

 16_046 137
 TCCAGCTAC TTGGGAGGCT AAGACAGGAG AATCGCTTGA ACCTGGGAGA C
 A/G
 GAGTTTGAG TGAGCCGAGA GTGCGCCATT GCACTCCAGC CTGGGCAACA
 AGAGTGAAC TCCATCTCGA AATTAAAAA AGAGT

 16_047 106
 GGTGAGGAGC CTGGAGCCCC ACGCTGGGCC CGAAGGTTCA AGGGCTTCTC ATCAG
 C/T
 GGCTTCTCAT CCGTCTCACC CTGGTCTGCG GCTTCTTCTC TAAATGCATT

 16_048 111
 AGCTACTGGA TGCCTGGGT CCGCCAATCT CCAGGGAAGG GGCTGGTGTG
 A/G
 GTCTCACGTA TTAATAGTGA TGGGAGTAGC ACAAGCTACG CAGACTCCAT
 GAAGGGCCAA

 16_050 133
 ATCAATTTGC TGCTGTTTAG TAAGGTATAA ACTACAGTTA AGGTTAAAGA
 CCTTGCCACA TTCTTTCCAT TTA
 C/T
 AGGGTTTCTC TTCGGTAGGA ATGATCTGAT GTTGAGTAAG GTGCAAACTA
 TGGTTTAAG

 16_051 145
 TGATCTCTCC AAGGACTGGC CTGGAAGGGA CAGAGAAATG CGAATGCCCT
 TT
 A/G
 AAAGTACTCA CAGCGTATAG TTGAGTGGTT TCCAAAGACC CCCTCTATGC
 TGCCAAGCCC TAAGCATGCT CTCGTATCTG TTGTTGGGAG AT

 16_052 98
 AAAGTGCCAG GGGTTGGCAT GAAAGACCCC CACACCCTGC TGCCTGCTGC

Table III

A/G

GGAATTGACC AGGGCATAGG CTTAGAGGGG CCTCATCAAT AATAACC

16_053 125

CTCTCCCCAC TAGGACAGGC ACGTGTCTC ACTAGGACAG GCACGTGTC

T/C

TCATTGTGTG TAGGTCAACA TGGAACTTTC TCCTACTGCT TGCTTTGGTA

AGAATGATGG GTTATCGGGA GGCTG

16_054 116

CATCTTGATG CACCAGGGTG GTCCTAATGT TCTCAGATAC ATTAGAATCA CACAAT

A/G

TGGTCCCTAA ATGAGAGCCA ATTCTGTCTT GTCATCAACC AGAGAAACAG

CAACTTGTT

16_055 113

CCTTGCAAGT CCCAGAGATG GTTAGGGAAG AGGGACTCCC AGTCAGCAAC A

A/G

TGCGATCTTG TAGTAAATGC CAGTCTCAGC TCCAGGTTTG GTTTGACCCC

ACATGTGTTG G

16_056 131

TGAGGGTTCT GTGCTTTTCT TGCTCCAATG CTGAAGAATG GCCTGCTGCT

TTCCCAGGTG TCACGGGCAC TGAGAAAGGG CCCC

G/A

TGGCACCAGG AGCTAATCCT CAGGGGTCAG AGGCTGTGGG AGATTC

16_057 139

CTGGGCTCCA TCCTCCCTCT GGCCTCACCT CCCCAGCCAG CCCAGG

C/T

TGCGCCAGCA TCTTCTTCCT CGTCCACACC CTGCCCTGCC ACTTCGCTCT

CCTTCTCTCT TGGTCCCTGC CCCGTTTCTA GCATGCCCC TT

16_058 143

CTTAGCCTCA GAGGTGTGCA TCTACTCACA GAAGGGCTCA GTGGCTTCCA

GTGTTCAAGG TTACTGGATT GCACA

G/A

GAGCTGTTAT AGGACAAGCC CCGTGGATAC TGGTGGCTCA GAGGTCTTAC

AGATGAGGTT TCACTGG

16_059 138

GCTTTCTGTG TGACTIONTCT TCTAAGTCT GTATAGACCT CCAGGCTTTG CCT

C/T

TCCATCCTGC CAGTGACACC AGGACTGCTG CCACCATTCA TGCTGTGCGG

ATCATTATCA TCCATGTCAC CTTTAGGGCC CACT

16_060 117

CGGCCAACT TAAATTTTAA AAAGAGGAAC AGAAGTCAGC CAGACCAACA

AAAGAGCGAC

C/T

GGTGTTCCTA GCATAGGAAA CAGAGGAAAC AGAGGCCAAA ACCTCGGGAC

TGTGGA

16_061 125

GAGCCAATGG CCAAGAAACA GTTAATAAAA TAACAGACGA TGGTCCTGGC

CTCTACTGTG AGTGAGTAAA G

A/G

Table III

GCTTGCCCTG CAGAGATTCA GTGATCTGGC GGGGGTTGCT GAGCTATGAG
GAA

16_062 100
ACTCTTCTTT CTTGTCCCTC TCATCTAGGC ATGGCCATGC CTCTTCAT
C/T
GACTCCTGTG TGTCCCTCC CCATTCTTGC TGTCAGACAG CGTGCTGGTT
C

16_063 140
ACTTACAAGT CTGGGGTCCG GGGCTCCCCG GAGCTGGAAG ACCAAGGCCC
CTGTGCCTGG GATCGCTGGG TTA
G/A
GGGCGGGTTA ACCTAGGGGT CCCAGCCTCC AAGTCTGGGG AGGATCCGGG
TTCACGGGGT CGGAGT

16_064 119
ATAAGTGAAT TCCGCTACGA TGGCCAACCT CTGCCAAACC CAACCTGACC
AGTGGCCAAC CTGAGCATCA CG
G/A
TGTTTCAGCCC ACTGATGGCT GCCTCCAGAT GCTCCCTGAA GGGACA

16_065 141
TTCTCTGCTA AAATATTGCC GTCTCAGTGA ATCAGCTCTA GATGAACTCA
TTGGGTGATT GTAGGAGAAG CCCCTCCCTT TGGGGCTTGG AGAACC
C/T
TGGGAAGGAG AAAGGACAGG TGGTGGGGAG AGGTGGGTTT CCCT

16_066 112
GTGACTGTTT CAGAAGCTGC CTACTCTTCT AGTGCCTGCA GCAATC
C/T
GAGGTGTGGA GGGCACTCCC ATTTCCCTTC CCTGTGCTTG AGAATCTGTA
GAAATTGTGC AACTT

16_067 119
CCACTCTTTC CTCTGGCTTC AAGTCACAGT GTGCCAGCAT CCACATGGGT
AACTCAGGGA TGATG
A/G
AGCTGGTCCC TGACAGGGCC TCACACCTCT CGCTGGTGGG CACTGACCTA
TCC

16_068 123
ACCAGCTTTT CCCCAGGGGC TTAGCCCAGG GCCTTTCCGG CACCCAGAT
C/T
GCATCTTCTT AGCTGTGCCC CAGAGAATGA GGTGAGATT GTGATCTGAA
ATATTTTCAA GGCAGGTGCT GCT

16_069 113
CCAATAGCAC TGTGCTTGAA TATTAGATCA AGAAATGGCC TGACAGCCCA
AGACCCCTTC TCA
A/G
TGAAATTAGC TTGAGACTTC TGACAAGAAC GAAAGTATTC TGCCCAATG

16_070 106
CCTCCAAGCC TCTGCACCTT CTGTTTCTTG TGCTCAGGCT TCCCTCCACC
TCCCACCC
C/T

Table III

TTTGTCTCA TGGTTGATGC TTCTTCTCCT ATGCCATGTA TTCCATG

16_071 115
ACACTCATAT CCACCTTTAT CCTAAGTCCC CAGACCTAAC TAATGCCTTC
TCAGT
G/A
TCACCCAAAG CCTAGGTCTT CCCTTATTCC ATGGGATAAC TGCACACAAA
ACCAGGATC

16_072 122
ACATGTTTCC TCTCCCACTT AGTTGGGGCC AGGCCCTGGG GAAGAGAGTT
TGCAAGAGGC CCAGGTTTAG
C/T
TGAACACGTG GAACCATTGG TGAGCTCCTA GCTCCTGCAG TCCTCTTTCC
A

16_073 138
ACTGCAGCTG CAGAATGACA GAGGCCATGT CCAAATCCC TTAGAGACAC TG
C/T
TGTCTTAGAG TTGTTAAAT AAGAGCCCC ATATCAGGTT TAGAAAATAC
TGTCACCGAA CGAACGTCGC TGCTCTCAGC TCCAC

16_075 100
TTTTAAGCCA CTGAGTTTGT GGTAATCTGA GGACCCTGGT GTATG
A/G
CAGATGCAAT TGACAGCAAT AACAACTTAA GCATACCCTG TATGGCAGAC
ACAC

16_076 143
TGACTCGGGC TGGGTGTGGA TTCTCACCCC AGGCCTCTGC CTGCTTTCTC
AGACCCTCAT CTGTCACCC
C/T
CACGCTGAAC CCAGCTGCCA CCCCCAGAAG CCCATCAGAC TGCCCCCAGC
ACACGGAATG GATTTCTGAG AAA

16_077 146
CTTGGGGGAA GGTGTCATGA TTGAACACAG AACTTAGATC TGAGCTTCCT
GGCAGC
C/T
GATGGAAAAA GGCAAATCA GTGAGCGCAT GGCTCACATT CACTCCTAAA
AGGCAGCACA GATGAGATCG TAAGGCAAAT GGCTCTGCA

16_079 145
TATGAAGATG AAATCAGCGA TTCCAAAGCA CAGCTAGCTG CCATCACCTT
GATCATTGGC ACTTTTGAAA GGATGAAGTG CTTAGTGAA GAGAATCA
C/T
GAACCTCTGA GGAATCAGTG TGCCCTTGCT GCATCCAAAC TTCTAA

16_080 145
ATCAAAAGCC CATAGCAAAT TCTGTTCTGT TCTTGGGGAA GCTGACAGTC
TGATTGGAG GCAGAGGACC CCAAATACAG GCAGCCTTCA CC
A/G
ACCCTGACTC AGGCAGTGAT ACTGCTGATG AATCTGTGGT TCCTGCCGGG
AG

16_081 121
AGCGTCTAGC ACCTGGTACA AACCGATGGC ATCTCCAGG CATTTCTGAA
CCATTTTCAC.

Table III

A/G
 TGCTCTACT CTCCGGCCGT CTCCACACCA CCCTGTGTTC TGCCAAAGGG
 AGCTAAAATG

16_082 144
 AAATTCAGGG TTTTCACAAA CGTAGTGAAT TTTCAGCTTG TAATTTGCTG
 TCTCCGGTGA GCG
 C/T
 GGTGCTGAGA AGACCCGTGA TGCTCTCTTT GAAGCCCATT TCGGGCATGC
 CCCAGGCCTG GGACCTCCAT TAAGCACCAG

16_085 131
 AGGAATTCAG AGCTGAAAAT GACAGGAGAG CTCCTCTGGC CATTTTACGG
 ATGAA
 A/G
 CTAGAAAGAG CAAGATATTG TCCAATCTTA CAGGGGAAAT GAGCAGAGCC
 AGGAATCTCA GGCTTGGAGC TGGGC

16_086 149
 TTGAGCCTGG GGGGTCCCCT CGCCAGCACA AGCGCCGGTT GGCAGCAGGG
 CTGGGGCTTT CCCTGAGGAA GGGGAGGAGG TAGCCCTGCA TGTGAC
 A/G
 GCGTGGGACA GTCCAGGCTG CACCTCCTCT CTCCAAGAGT GTGTCTGCAG
 GT

16_087 145
 GCAAGGGAAA AGATGTATCA ATTTTCTCTA TAAATGAAGA GGCTGTTGCA
 TGGATCTGAG AAAGCCATGG GGTGAAAGGG GACAGGCCTC C
 C/T
 TAATGTTGAG TGACAGAGAG AACTGCAGTG GTAATCGTTA ACCAAACCAC
 CTG

16_088 149
 AGTCCGAGGG ATGTAGGTGA CAGGGAGGCT GCTCAGCTCA GCCCTGCCTG
 CCTGC
 A/G
 CCACCCAGGC TCCCCAGGG AGGTCCAATC TCCCACCCAA GGCAGGACAA
 GGCAGACGAG AGCCTCACGA CACCGACAGT GACGCACACT TCC

16_089 139
 CATGACACTG AGTGAGGGGC CCCTTAAGGG CTATGGGTAC AGGTAGG
 A/G
 ATGCTAGTTG TGGCGAAGAA AGCTAGAGCT GATTAATTAT GCAGGCAGCC
 CCACCTCTGC AAACCACCCA TCTGGGAGGT CAGCCTGCAA A

16_090 124
 GGATGGGGGA GGTGGCCCTT AATTCTGCCT TGAGAAACCC CGCCTGAGGC
 CTCAGCACCT CCTTGTCCAG CCACCCACA
 A/G
 GTGAGGGTCA ACTCAAGTGC CTGAGTGTCC TCTCTGCACC CTGA

16_091 136
 TTTGGGGCAG CCAACCTGGC ACAGCTAATC AAAGACTGAC ATGGAAGCCA
 CTCCCTCTCC CCTCCCCTGT ATCACTGACA CCATTTTCC
 A/G
 TCGTCTTGTC ATCGCAGACT TTACAGTTGT TGTCATGAGT CTAATC

Table III

16_092 108
 GTTCATGTGT CAATTACCTG GTTACTTAGT AACCAAGTAA TCCAGTAACC
 AAGAAGTCAA GCC
 A/G
 TAGATTAAAT AGTCCCCAAC CGGGCAATAA AAAGGTCCCT GAGTACAAAT
 TTGC

16_093 85
 CTACAACCCT CAAATTCAAG TGACAGAGCT GGGATTTTGC AC
 A/G
 TGCACATCCA TCAGTTATTG AATAAGGCTG CTCTGAAAAG GG

16_094 149
 ATCCAAGAAA TTAGACACAG CCCTAAGAGA AACATGCAGA AATGAGCAGA
 ATAGACCCCA AATAGATCAA AATTCTGTCC CACCCTCTGC C
 A/G
 TCCCTCTCAG AATGGAAAGT CAACAGCAA ATTAAGTTTG GTGGTGAAAA
 AATAACT

16_095 119
 AAGGGAAAGG AAGAACATAT GGGGAAGGCC AGAGTGGAGA CAGGCAAACC
 AGAGCCTGAA AACGAAGC
 A/G
 TCCTCTAGGT TAAGTTGAGA GTGTAAACTT TAATCAGAAG GCAACAGAAC

16_096 137
 TGCCCTCCAG CCTGGGCTCA GGTGACTCAA GGGAGAAAGC ACCT
 C/T
 CCTCTCCCCG CCAGGGAGGT CTCGCCATGT TTTGGAATCA GTACCATTCC
 CTTGGGGCTG GGGGGCAGCC CCCATCTCTG GACCTGGCTG GA

16_097 126
 AAGTTGTAGA TGGCCAGCTG GTACCATGGA GTCTAATGAT GCCTCATCTG
 TCCAGTGCTG ATCTTCGACA TTCCC
 A/G
 TGTCTGGGAT GGGAAATCCA TTTTGTAGAA CGAAAGGAGA CAGAAGGCAA

16_098 130
 AGATGTGTGG TCATTATCAC ACCGTTTGGT TTAATATTTA GCCAATGTCT
 TGGTCAGGGA GCCTCGTACA ATGGCTCTCC ACAATCCA
 A/G
 CACTACGATG ACATGTCTTT CTAACCTTCC AAACCACACT G

16_099 137
 GGAGAAAGAA AAAAAAACC TCAATTTCCC AGTGAGCTCA CTGCTTGCCT
 CTCTTTCGAA GTTCCAAATT GCCT
 C/T
 CACTTTCTCA GAATTCCAAT CAGGGCTCCT TCAGAGGAAG CAATTTCTGC
 CAGCACATGG TC

16_100 148
 ATTTAGGATT CCTTTGTTCT TGGAAAAGAC AGTGGCCTGA TTTTAGGAGC
 A/G
 GCATTTCCCTG CTGCCCAGCC TGCCATTTCT ATCACAATGG TAGTCAGTGA
 GGGTGAATGT AACATTGCCG TGACTGTGAA CAGGAGGTAG CCCCATG

16_101 133

Table III

CACAGGTTTT GCCTGTTTTG CTCTCAGATG TGCTCTAGCT CATAAGACAG C
 A/G
 TCAGGCATAC AGTAGATGCT CAGTAAATAG TTGCCAGTTG TGTGAATGTA
 GAACCATACA TCACCACAAT GCTGTACTAA T

16_102 133
 GCTGTGTCTG CCGAGCCCAG CGTCCTCACA CAGCCCTGCT GCCACCCAGC CA
 C/T
 GCTGGCCAC ACGTCCCTTA GACAGCCGGC CACCTCCCGT CCCACCCCTG
 CTGCTTGTTT TGTGCCCTCA CAGGTTTGCA

16_103 144
 CACTCCTGGA TTTATGTGAC TCCCTTAGCT ATACTTTCCC AGCCCCCTGG
 GATGTTCCCC ACTCATCCTA TTCAC
 T/C
 CACAAAGAAA TATTGTCAA ATCAATTGGG TGATGATTAG GAGCCATTAT
 CTGCCTGCTG TGCTGAAA

16_104 139
 CACCTTGCTC TCATCTTTTT ACTCCTTTAA TGCTGACCTC TGCCAAATTG
 AATGAT
 A/G
 TATTTTCACA TCCTGACAAA AGGAACTGAC CATAGCTGAT AGAGCCCCAC
 ACCTCCTTAA AGAAAATGTT TTGTGAAAGC TA

16_105 128
 ATGAAAGCTG GGTGGTCTTT GGGTAAGGAC AGGGGAAC TA GGAGGTAGGG
 TGCAGGGTAA TGATTTGCTA CCC
 C/T
 TCTTTCTGGT AATACCACCA CCCTCCCTTC CTAGTTTCTT AGGAGGCCCT
 TGAT

16_106 100
 TCTCCTGGGG AAGAAGGAAA CTAACCTCTT CCTATCCCC TATTTAATGC T
 A/G
 GCATCTGCTG TCCTCTGCTG TGGTAACAGG GAACTATCTC CCAAGGAG

16_107 141
 TGTGGGGCAG CTGGAATCGG GCAGACCTGA GTGTAACTC AAGTTGGCCA
 CTGC
 C/T
 GGCTGTGCTG CTTCAGGCGA TTCTGTTGAC CTTTCTGTGC TACATAATGA
 AAATTCTTAT TTTACTGAGT GCAGGGGCTG GGCGGG

16_108 107
 GCCTCAATGA ACGACATCAG CGCTTCTCTA GTTGGTGAGA AGGCCAGGA
 AAGCTTGGTC TG
 T/C
 GTCATACACT CAATAGCTTC TCCTACCCAG CCACCTACCC TGCC

16_109 137
 TACTTGCTG GCTGCTCATG GTTAACAGAA GCCCAGGGAG AAGCTGACTC TA
 C/T
 CTTCTCTTCA GCCACACCCA AGATATTGGT ATAAGGGAGG CTGGCACCAT
 GAGTATTAGT ATAAGGGAGG CTTCCGGGTT GTGC

16_110 142

Table III

GAACCTATT GTGAAGTGTG CACGCAAGGG AACTAGGCTG TGCTCCTTA
C/T
GAGAATCGAA TGCCTGATGA TGGGAGGTGG AGCTGAGTTG CTGATGCTAG
TGCTGAGAGT GGCTGCAAAT ACGGATTAAC ATTAGCAGAG AG

16_111 121
CTACTGGGTT TACATTGGAG ACCGTCCCAT TTAATTCCA GGGTG
A/G
TGGGACAAAA TGGGCTCAGT TCTTACATAG CACACTACAC ATGTTTAAA
ATACAAAAT TACATTGTTG CTCCC

16_112 109
TCATCATGGT GATGGCATGC ACCTTTTCA GGGCCGGAGC CAGTTCTTG
AGGAGACTCT GC
A/G
CAGGGCATGG ATCACTGTGG TGCCCTTTTC CTGTGCCTGT GCCTTC

16_113 108
TTTACATTCT CTACCCTGTC ACACAATATT TCACAAGGGA ACCTGGACAA
AGGGAAT
C/T
GGTGGCAGAA GGATGCTACC CTGCTCTT ATGAGCTCCC ATCACTTCA

16_114 139
GTCTCCTCAG TGACCATAAT GCTGAACAGT TGAGTTTCT CATTGTCCCC
TATTA
C/T
ATCCTTCACC TCACAACTCT GTGGGAAGAG CAGCTGCAGG GTGCACTGAA
TATTAATCTC AAAGCAGCAG GCTGATCAGG GAA

16_115 128
TGAAAGTCTT TCCTGGGTGT CCTATAATGC AGAGAGCCAA AATGATCCTG
AAGAAGT
A/G
TCTGTCCCA TGCCTCATCC ATAGCATCTG CCAGGCCTCA CTGAACCAGC
AGAATCTAGA CCTCAGTCTT

16_116 129
ACCCACTGCG TTCTGTTTTT TAGTCATCTA ACATACTTTG CAGACTTCTA
GTCCCATCGA TACAGAA
A/G
GGAGTCTACA AAAGAGTAAA TGTGAACCTG AGAGAAAAGT GTCCCCATCT
GGCACAGATA A

16_117 123
CAGCTAGACA CCATAACCTG GCTCACTGTC TGGCCTTCAA GTTCACTCA
GCAGA
C/T
AAATGCACCC TTAAGTAACC TGGTAGGGAA CCTGTCACTC TACATAAAGA
ATGTATGGCA TGCCACA

16_118 141
ATCGGCGGTG CTGAGCCGTG AGGTCCCCTA CCTGCCCTGT CAGGCAAAT
A/G
CTTGTGTCAG CATACTTCTT TCATCCGTCA CTCAGCCAGA GTCTGTAAGA
CAGACTCAGC ACTAGGTCAC ATTTTGAAAG AGAAAATAGA

16_119 105

Table III

GAAGATTTTT CTTCTCCTC CCCCTGTGAC CAATAGCCAA AGACATATTT
TGGGATG
C/T
ATTAGTGCAC TGGGACCTTA CTCAGTCTAT AGATGACCAA GTTCACA

16_120 133
AAAGGAGAAA TACCAGTATC CGTCTTAAGA GCTGCTCTGA CAGCAACTCA
CAGTTCTGAT AAACACTATT TAAGTGCCTT GTGAA
A/G
GCCTTTTTTG GGGAGGCTGT CAGCGAAGCA AGTGAGACCA TGTGATG

16_121 145
CAGTAAATCC AGGGCAGATG TATGAGGTAA TGAAAGAAAA TTTAAGAATG
CACTCACACA TTGATGTGAG AACTATTAAG ATCCCCTTCT CTCTCT
T/C
CTATACCTCA AGTTCGTTAT CATGCACTCC AAGCTACCAA ATATTCCA

16_122 141
CGGGGACAAA TTATTCACCA ATCTTCATCC CAGGCTCAGA GGAAGATTAT A
T/C
ATCCAAGTTT TCCACTATAA TTAGGTTGGA GCCATATGAC TAGGCTCTGG
ACAAAAGGAC AGTGGAATA CTAGGCATCA CTTTtaggc

16_123 130
TAGACAAAAG GATGAGATCT TGGTGTGGGG GGTAAAGGA TGAAGCTTTT
TCGATTCTTC TAGCATC
A/G
TGCTAGACAA ATTCCAGAAA CAAACTGGAT GCTTATGATG GAAGCAGCAG
AGGCAAAAGA GG

16_124 127
GCTGGAATTA CACTGTGATG AACTAGGTTC CCACACTATT TGGTGGGAGT
GAATGAGAGG CTTTGGATGT GAATGT
A/G
GGTGTGCCTT GTTCACCTTG CTCAGGTTCC AGCAGGTGCT CAATAAATGT

16_125 119
CTCAAGTGCA CATGAAAACC TTAAAGTCAT TACAGAATTG CTAGTCCACA T
T/C
TAGCCTCACA GTTAAATTTA ATAGTTCATT TGTGAAATTA ACAGACGAAT
TTGTCTCGCC TGCTAGA

16_126 105
ATACCATAGC CACCCCCGAC ACCACCACCA GATTTC AAG ACCCCGGACC
CAGCACCC
T/C
GAAGGGTCTC TGATTCTGCA CTGGAGCAGT TTCTTCTCCC AGGCCC

16_127 136
CTACTGAATC AGAAACTCTG GCAGTGGATT TCAGTCCTCC AGGTGACTCT
AATGCAC
A/G
CTCAGGTTTG AGAAAGGATC CCTGCCCTA ATCCATCAAG CCAGGCCAGG
AGAGTGCAAT CGTAGAGTCC ATGTGTCC

16_128 139
GTTTCGTTGTG TCTGGTACTC ACTCTGTGTG CTGCATCTCA CTTTCATCAT

Table III

C/T

ATGACAAGGT GTGCAGACAA GGAAGAATGT TCCTCTGGGC TGCTTACTGA
TAAGAATCAC ACAGTGTAAG CCTTTCAAGG GAACTTAGA

16_129

131

TTGCTATCAT GTAGCTAGAG TCGATTAAGT GGCCAAGGGT CCAAGAGACA
GGTGAGACCA TGAGGAGGCA CATT

C/T

GATGTGATGT GACCACAGAA CCCTGGGTAG TCTCAAGGGT AGAAGCCCTG
ATGATG

16_130

119

GCGGGCCATT TCATTGGCCT ACTTTTCAA CATCGGCTAG AAAGGCCTTC
AAAG

A/G

AGGCTTTGAA AACCAGCCGG CCATCTTCAC AATAAGCTCA GACGGTTAAA
AGCCACGCTC TGGA

16_131

142

GCTTGGATTT ACTGTGTTCA TTTCTCTGAA GCTTTTLAGA AATACCTGAG
GAGG

C/T

TGGGCACGGT GGCTCACGCC TGTAATCCCA GCATTTTGGG AGGCCGAGGT
GGTCGGATCA CCTGAGGTTG GGAGTTCGAG ACCAGCC

16_132

144

TTCCAGATT TTGTCTGGAT TCTGCCTGCT AGAGTGCCTC ACCTTCATGA CC
A/G

GCTGTCACCC TTCATTCAAT TGAATGCCAC AGCTCTCTCC CCACACCCAG
GCCTTTCTTC AGTCTCCTCA TGTCATTCT CCTCCAGGG A

16_133

122

AGACCCAGGT GATTTTCATA GGTATTTCAA AGGCAAAGCC AGCTCTGGA
A/G

ATCAAAGCCC TGCCCATCCT TCTAGGACTA GGAGAACAAG TTATTTCCAG
ATTCAAAC ACACATGAGT GT

16_135

138

TGGCTGGCCT GAATATATCT GGTTCGTGC GGACAGACTC TCTTTGGCTC
ATGTATACCT TCAATTGCAT AAGGGAGAGA ATATAGAGGA C

A/G

TTCCAAAGGA AGTGCTGACA GACTGCGCCC ACCTTGAGAA GGCCAA

16_136

129

ACTGTTCCAT GGGAGAGTAT TTTAGAGACG ATGGCAAATA TACTTTG
A/G

TCATCTATGA CGACTTATCC AAACAGGCTG TCGCTTACTG TCAGATGTCT
CTGTTGCTCC ACCGACCCCC CTGGTCGTAA G

16_138

147

GGATCTCCAT GTCCCACTCC GCCAGCTTCT GGGGCGGCAT GGGGTCTGGG
GGCCTGTCCG C

G/A

GGGATGGCTG GGGGTCTTGC AAGAATGGGA GGCATCCAGA ACAAGAAGGA
GACCATGCAA AGCCTGAAGT ACTGCCTGAC CTCCT

16_139

131

Table III

CAGCCTGTTA AAGGAATTCG ATACCTCCCT CCCTCCAAAC CCAAATCCAC ACCC
 A/G
 CTTCTCAGCT TACCAGGGGC ACAAATCCCA CTGGCATCCT AGAGGAGAGC
 CTCAAATCGT AGGAGGCTGG CTGGGT

16_140 133
 GAGACCACCT CCTGTCAGCT CAGGCTGAAG CTGAGAAGGG GAACCTCTGG
 ACAGAGGGAG CTC
 G/A
 GACATCCTTG ACTACAAACA TCCTGACCTG ATTCAGCAAG TGGTCTGGTT
 TCCCCTGGTG GCCCCAGAA

16_141 124
 GCTGACACTG CTCTTCCCGG CAGCAGGGCT GGGAGTCCCA GAGCAGAGAG
 GCCTCCTCTG AGTCCCTGCC GTGTCC
 A/G
 CAAGCTCATG TCTAAACAGG AGCTATGCCA AGCCCCTGGT TTCCGCA

16_142 99
 GGGTGGGCAG GGTCCCTGGGT ACGTCATGCC TAGGGGCAGC CTCAGCAGCC
 CA
 C/T
 CCCCCTCTG ACCTCTGAGC CCTGACCACA GGACAGCAGC GGCTTC

16_143 115
 CATCACTCAG GGACAAGTCC CTCTGGCATC CCTTGTGGCA CCATCCATTC
 CTAGAGAAGC CAGGAA
 C/T
 GTGTGCACGT GAATGAGGGG GCAAAGCCAA GCAGAGGGCT CTCTTCTG

16_145 136
 AGAGCCAGCT GCTGCCAGAA GCTATTACTG TTATTACCGG CCGGCAGCAC
 AGGCTACAGC CACAATC
 A/G
 TAAGAGGGAA ATGGACTGAA TCCCACACC CCAATCCCTC ACTCACTCCG
 ACCCGAGGCT GTCTACCC

16_146 137
 GGTGCGGCC AAGGTTTAGG AGCCAGCACA GAAGCCTCTG AGAGCCATAA
 GGGT
 A/G
 GAAAAGGTTA CCCGGTACTA AACCAGCCAG CTCGGGGTG ATCTCATCCA
 CTTCCCAAGA TAAGCCCCCT CCCCCACCCT CT

16_147 123
 GAAAAGGTAG CAATTCCTC CGGGCTGAGG ATACTCCCAG TAAAAGGAAT GGTG
 C/T
 GATTGTGGGC CCTGCTGTGT CAGGAAGTAG AATCAGATGG AAGAAGTTTG
 TTTGGGATGA CATGAAT

16_148 148
 AATTTTGTT TGGATCTGGG TAACCTAAGA GGAAGAGAAG ACTAATCCAA
 CTGCCACACT CTTAGGCCAA GCCTGAATTG TCAGGAT
 G/A
 CCAGAGACAT AATCAGAGGG TATCGATAAC TTGAGTTACA CCAACACCAA
 TGGGTCAGAG

Table III

16_149 145
 TCAGAGACAA AGCTGAGGAA TAACAAGGAT GACTTTTCTA ACAATAGATC
 TGATGAAGTA CTGGACCAGC CAAGGGAATA TCGGACA
 G/A
 CTCCTTCCTA GACATTTGCT GAACAACTGA CTTTAGATGA AGTCCTACTC
 ATAGGTG

16_150 142
 AGCCAGACTG AACAACTGT AATTCGTCAA ACATATCAGG TGAGG
 C/T
 GTGAATGTTT TATTCGGCTC CAGGTTCTGT GCATGCTGTT CCCTCCTGGC
 AGGTTCTGTC CACCCCTCCC GCAAATACAG GTAATCTCCT CAGGTC

16_151 133
 TTCCCCGACT CCCTTGTATC TTCTCCCTGC CTTCCAACAG AGAGGGCAGC
 AGCCTCTCCC AACTGGCT
 A/G
 ATTCTACGCC TTGCCTTTGA GGGTTACTTC ATTCACTAAA ACCGGTTCCT
 GCTGCCCCTG TTCA

16_152 108
 TGGGGTACCC CTGGGGGAGA AATGGGGAGG CCAGACCCAG CGGTAAGCCA
 GGGGGA
 C/T
 GTGTGGAGTC AGCACCCAGT GCTGTGGGAT AGAGGGATCG AGTCTGGCCT
 G

16_153 146
 CGCGCACTCT ACGCCTTCAC CGGCCTGACC CTCACGCCAC AGCTCGAGGC
 CTGGATCCAC AACATCACCC ACGGGTCGGG GATCGGCAAG CCAATCGA
 G/A
 GCCTTCCATA CTTCGTCTAG GAATGCGCGC AACGTCTCCC AGGCCTG

16_155 145
 TCTCCAACCC TCAGTGCTGG GGGAAATGGT GCTTCATGTG TGCTGGG
 A/G
 TTGTCAGCAC TGGCTCAAAG ACTGAGTCCA CTAAGGATAC AGAGCAAAGG
 TACTCAGGAC CAGCACTAAT GAGAGATGAG AAAGCCAAGG CTGGCAG

16_156 117
 CAGGACTCAT TAGCAGGAGC TCATAAAATG AAAGTGGCAG TGAGCTCATA
 TGGAAGA
 A/G
 GCATCACGGG CAACTCGGCT TGGCTCACCA GCCCCTGAGC TGCCCCCGAG
 TGACCGCTCC AGCCTTCTT

16_157 124
 AGAGGTTTCTG GGTCCCTATG GGTATCACAG GAGGAGCATA TTCAGAG
 A/G
 GGTAAAGA GGACATGATC TTGAGGTGGA ATAACATGGG TGCCAAAAAT
 TGAGGAGTGG GGTGACTAC AGGGAG

16_158 149
 CTAACTGTC TTCCCCTTGG CTTCAACCCCA GACTCCTCTT CCACTCCTGA
 TTCAGGAGGA AGCCTGTTCC
 A/G

Table III

CCTGCATTCC CCATCGCATG GTCCAGCCAG CCTGTACCCT TCTCTGCCTC
 ATCCATCACC CGTTCTGCCA GCATGGGT

16_159 141
 TGGCTCCTAG AAATACTTCA GATGCCATGA GATCCACCAC CTTGAAATGT
 CAAAGCAGCA AAATTCAAAC CCAGGGGCCC TGGGTGCCA
 A/G
 TGAGACAGCT GTTATCTTTT TTA CTCACCA GACGAGGTCA CAGATAGAAT
 G

16_160 142
 CTCGTCATTT GTGTGCACTA AATTTTGAGA ATCACTAGAT AATTTTCAGC
 TCTGCAGGCA GTTCCTGCTT C
 C/T
 ATCACATGGG GCCTAGCCAA CAACTTAGAA TTGAGACAAA CAAGTATCTG
 TACCTTGGGT TGCCAGGAG

16_161 116
 AAGCCTTCAG GGGAGGCAGA ACTAGGAGGG CCCTGGAAGT CAGGGGGCCT
 GGGATGGA
 T/C
 AGCCCTCTGT GGGCCCCCTCC ACTGGGATTC CCAGAGGCCT TGCCCCCTATT
 AGTGCCGGGG ATGGCCC

16_162 112
 CAGAAGGAGC GGGCGGGACT GGCAGAGGGC CAGCATCCTG GGAGAGAAGG
 GCTGGGCTCA AAGG
 C/T
 GAGAAGGCAC AGATGGCACC CGTGAGCCAC GCTGGCACCT TCGTGCT

16_163 146
 TGCTCCTCCT CCATAGAGGA GTTATTAAAG CCACAGAGTT AAAGTAAAAT
 GGCCCGAGAG CAAGACAATG AATATCAGAG AGGGTCACAG GA
 C/T
 ATCAAGTGGA CTTGTGACCT TGGGAGTGTA AGCACCTACA GTGGACAGAG
 GGG

165 141
 TGATAATGTC AACAGCTTTC GAGAGCCTCT GAGCAGTGAA TGAGATGATA C
 A/G
 GGTGAAAGCA GCTAGCGCCA TACCTGGCCC AGGACAGGCA GGAAAAATGT
 CAGGCAGATC TGAAGCTGAA TCCGGTTACT GAGTCATCA

16_166 125
 CCAGCAGGGA TTAGAGCCAG GGGCAGGTGT CATGGAAATT CCTTCCACCA
 C/T
 GGCCTCCACT TACTTGACTG GCCGGCTTCC TCTCTTCTGT GGGTTTAGAA
 GTCACCCGCT GGACACCGCT CCTT

16_167 106
 GCCCCCTCTG GGCCCTGCC TAACAGAGGG ACAGAGAGAG GGCTGTGTCC
 AC
 C/T
 CTGCAGCTCT CTGGATTTGG CCAAACCTGG CTGCTGTGTG GCCCATTCTT
 GGG

Table III

16_168 130
 GCTCACCACGAC CCTGTGAGTA CTGGCTGCGT CTCTGGGTGG CTCTCTTGTTG
 TCTGGTCTAG TGTCCCTC
 A/G
 GGTGTGGCTG ACCCTTTGGA GGAAGCAGTG CACAGGGACA TATTGACATG
 GGTGTGGAAC AA

16_169 127
 GTGTGAGCTG GTCCAGGCCA ACGGGAAGTG GGCAGGAACG GCATGGGTCA
 CTGGAAGGCC ACAG
 C/T
 GGGAGAGTAT CCAGGGGTGT TCCTGTGTCT GTTGCCCGTG CCCGCTGGTG
 ATGGGACATC AG

16_170 122
 ATGGTTTATG TCAAACCGGA GAATGGCCCA GCCCGGCCAG GGGCTCCAGG
 ACAGTTCCCA GGTGTCTGG
 C/T
 GGCTCCTACT TTCCTACTCA AGAGTAATTA GAGGGAACCC TTTTAAACC
 ATT

16_174 132
 GGGGCCCTTTC TTAGGAGAAG TTGACTTCCT GGTTTTGAGT TGAATGTAAC
 TCTCCTTTGC TGG
 C/T
 TTCTCCGCTC CCACCATTCA TTTCATAAGG ACAAGGTCAT GCACATTGTA
 ATTCTACGGG TCGGATCT

16_175 144
 TTGCCGCTCA GCACAGGGCG TGAGTCAGCC CCAGTGGCCT GAGGCGTGT
 TCAGTTTCCT GCTGA
 C/T
 TCAAGGGTCG TGAGTTTAAA ATAGACTTTG CCTGATAACT TGGAAATGAG
 GGAGATTTAG GCTGCACTTA AAATGAGT

16_176 135
 CCCTCTCCAG TGAGGGTGGG TCAGAGTAGA CCCCTGACTG GGCAGATGAG
 GAGGCTGCTC AGAGGAGGCC TCCAGC
 C/T
 CTCCTGCCT CACCAGCCTT GCTTTCCTCC CCTCTTCCAC GGGGAAGCGGA
 GCTCCTAA

16_177 119
 GTTTAATGAT GCATGAGGTC TTGACAAGAA CCTAAACACC AGCCTGTGGT TTG
 C/T
 TTTGGTTGTG CTGATGTCGT GCTGAGGTCA CAGCCCAGGA CCATGACCCC
 AGAGGCCCTG ATAAA

16_178 113
 CAATCTAGAA AGCGGGGCAA TGGGTAATCA GTCTCACCGT CACTAGGC
 C/T
 GAATGGGAGA AATGCTCCTG TGGACATGGC CTCCCAGTGT GGGTGAGCAA
 AAGGGCAGGC TGAG

16_179 139
 TGAAACATAC GGTGCAGGCA AACTCCAGTT TTCTTGCCCT GCAGGTGAGA CCACC
 A/G

GAAGTGCAGT ACTTAGGGCT CCAGGAGCCC CTCAGTTGCC CACAGAAAGTA
GCTGTTTAT TAACACACCC TCGATAACTT CCT

16_180 148
CCCATGAGAC ATGGAGGGCC TTTGAGAGGA AAAAGCCCAG ACCTGGCCCA
GCTCTGGGAC TCCACACGTT AGGAGGGGCT GAGGC
A/G
AGGAGCGGCC ACCCTGCCAA GCTGAGCCTT ACAGGCAGGG GCCATGTAGC
CTGCCGTCCA CCG

16_181 125
AAGGTAAGAT GACGGCAGAA CGTCACGGAG GAGCAGGGCA GGGCCC
C/T
GTTAACAGGC TGAGCCGGGC GCAGGTGAGC AGACAGCACT CGGCACAGGG
CCTGTCTAGA GCCTGCAGTC ACACCTCC

16_182 146
TTTCTTTGAG GGATGTCTCA ACGCACCAGG ACAGCACGAG ACGCCCAACC
CGAAG
C/T
GGCTGCTGCC ACCTGAGTGC GCCCTTCCAA CCTGAGGTCT AAAATGGGGA
AGAAAGCTGC ATCCCCATCC CGCTCCCGGG CAGAGCCAAT

20_001 110
TAGACCT TACTATGTGC CGTCCTAGTC GCGCTTCGTA TGTGTTAAGC
CCTTT
A/G
TCCCTCACTC CAATCTGTGA CATAGGCACT CAGTACCCCG TTGCCCAAAT
GAGGAAA

20_003 144
AG_CACTTTCGGA AGCCGAAGCG GGTGGATCAC TTGTCAAGAG
TTTGAGACCA GCCTGGCCA
A/G
CGCTGGTCTC CATAATACTC AGCCTATGAA GAACCAGGAG AGGGACCTGC
ACACTAGAAG ATAAATTGCT TGTTGTAAC GT

20_005 146
GATTGTCTCT CTGGACACGG CTTATGTTGA CAACCTGGAT CACATTAGAG
GATCACACTG AGACCTTTAT GTCGGCCTCA GTT
C/T
CTCCATCTGT AAAGTAGAGG TTGGGCTTAG ATTATAGATG ATAAAGACAC
CAACTTTCCT GG

20_007 112
G_AATACATGCT ATCTTGCTTG TAGAAGCCCA GATTCTCCT TCTTACGACT
CCCA
C/T
ACCCACTTAG GAGATTCTAT TATGTCTTAA AAGAAGTTAC ATCTCCATTA
GTGTCA

20_008 145
CAGGT GGATGGAGGC TGTTCTCATC TGGGGCTGTC TCTTGATTAA
GGCTGTCACC TGTTTGTATA GGGACCATGT TTCCCA
C/T
GCACTTTGAG TGCAGTTTAG GAGGTATCCT TTGGATGCTG AAGTGTGGG
ATTTTGAGGA CA

Table III

20_010 132
 ACAA GACTGCAACT TACATTCTGT AATGAAAGTT TCCATTCATT
 TGTTCACTCA ACAGTTATTG TATGCTAGGC A
 C/T
 TGTGACTGGA GTGAGGAATG CAGAGATGCT CAGGAAACGG TTTCTGCTCT
 CACCCCT

20_011 126
 GCA AGTTGGGCAT GTATCCTCGT GACCACTACA GATGTGCTAT CT
 C/T
 AATCGTGTAT GTTGAAGACT AAATGTTTTT AGTGTAATAG AACTTGACCT
 CAAATAGAAG ATTGCTTTTA

20_012 128
 TGTT TTCCATGAAT CATTTTTATG TTTTCAAAG GTTTACTCT
 TTTCTCTCTG GTAGTAATCA CACCAGGAC
 C/T
 CCTTTCATCT TGTACTTTGT TCTCCTCCAG TGGCAAGGTT TTGTGGTCCA
 GACC

20_013 145
 CTGTGGGA AGGGGCAGCT AAGGCAACTT GGAAGGGATG AGTATAAGGA
 AAGATATGTG GATGCTAAAG AATTGGGATG AAGAAGAAAT CTATG
 A/G
 ACCAGTTGCC CAAGTCTTTG ATAAATGAAA CGAGTGACCA AGATCTGGAT
 A

20_014 110
 TGCACACAG CTATACCTTC CTGGTTCCTG AGGATTGAGT GTCCCCCTGCG
 T/C
 GCTTAAAGCT GGAGCCAGAC GTATGCAGCT TTTTCCCGCT GTCCCCAGGC
 ACCGAGTACT

20_015 138
 TCAC TGCAGTGTCT GCATGACATA TGGATAGTAC AGAGACCTTC
 AACTATATT ATGATACAGA CCAGGAAAAT TAACATAGCC
 C/T
 TAGGGCAAAA CACTGAGTAA ATATTTATGT GAATGAGGAC TGTTTCTGAT
 CTT

20_017 140
 CCCT ACCTGTGGTT
 CCTTCTGCAC CCCTGCCCTT CAGATCTGTG ATGGGCAGGA CCAAAGAGCA
 GGCCGAAGAG CTGGAACCAC GAGCACAAGG
 A/G
 CCATCTCGGC CCACTGCCCT GTGATAAAAT GTGGCCCACT GAACA

20_019 146
 AAATA AGGTAAAGCC CTTGACCTCG AAGAGTTTTT AGTAGTGGTT
 GGAGGAGTGA GGGTAGAGGG TGATA
 A/G
 CTACATATAA ATGCATTATA CTATGAAAGG TATGTGGTGA AGTTATTGTA
 TTAGTCCATT TTCACGCTGC TGATA

20_021 142
 GAAAT GAAACAGCTA GAGATGTTAT GAAGGTATAA GATAATGAGG

Table III

CATAAATCGT ACTCAAGCCC TAAGGA
 C/T
 ACTCAGCATG TAGGATCCAT TAACAAAGAA GGGTTACTTA CTAAAGAAGA
 TGTTTTTTGG AGGGGTGCCT

20_023 126

GAG
 ATCCACTGCC ATAGAAAACG TGAATGATGC TCTTCTTTTA AAGGTCAC
 C/T
 AAGGACCTCA CATTCTTCAA TCCAATATGT ATTTTTCAGT TGCCATGGAC
 TTTACCATTA GACACCACTT ACCA

20_025 148

GGGGG TTAGGAAATG TCAATAAACG TGTCATAGCA ATTTTAGATT
 TTAGCAGTGA GAAAGTATGA TTTTAGTCAA ATCTTGAAGC AGGTGA
 A/G
 GAAGTACTTG CCAGGTTTCA GTGGGAGCCA ATCCCAGGCA GAGGCTACAG
 CAGGTG

20_026 138

CAGAGGAT TGGAAACAAC GATATGGAGA GAGTACAGAG
 CAGACAATGC TGTGCAGCCT TGTTTGAGGG CTGCTACAG
 A/G
 ATGCTATTCC ATTTGCTCTT CGGATTCAAA GTTCGGGTAG AGAGTCCAGC
 TAGCCAGGCT

20_028 139

TAAAGCCA TTCTGTTGCC TGCTTCTCTT TCTGTGGCTT AAACAGAG
 C/T
 TTGCAGTGGC CTGAAAAGTC ATCAGTCATG AGAAACAAGC TTTTCTAAAC
 ACTAGGCCAG ACAGAACAGA TTAGGAAATC TCCAAACTGG AT

20_029 118

AGG GAGGAGGGTA TGGGGAAAAA TTGATGGGGA AGCCCCCAG ACTTTTGCCT
 TGTGCCCAGG ACAATGACTT
 C/T
 TCAGCCAAGC ACTCAAACAG TATGAAGCCA ATTTGCTGGG TTCA

20_030 136

TTT TGAATCCCAG ATAAAAAAGG AAAATACATC TGGCACTTCT
 CCCTCTTTGC CATCCTGCCT TACTCTCACT TTGAATG
 C/T
 AGATGTGACA TCTAAAATTT CAGGAGCCAT ATCACATCCA TGAGGCAAAG
 GTATA

20_031 137

AGAGGGG TTTAGAAAAG GTTGCAATGT ACAGAGGGGT TTTTAATTTG
 TATTAATATT TCTCAGTTTA CTTCCCTC
 C/T
 ATTTAGATTT AAGATTTACT CATTAATTCA ATAAACATTT ATTGAGTGTC
 TGCTATGTAC CA

20_032 146

CACCTACGG TTGCTGCAAT CTCCTGCAGC ATTTGTACTG GTTGGTATCA
 TTTCTCACT ATTGATTCA
 A/G

TTACCTTATC TAGGTCCTTA GGACAAGAAG TGAGAAATAT GATACCCAAC
TCTAAAGAAA GAGGTTTGA AGGGAA

20_033 135
CATT CACACATTTG GGTGGCTTG GTGGCTCCAC ATTCATTACA GGCTAG
C/T
TCCTGGGGAA CCTGGGAAAT GTAGTTTTAG CTTTTTGTCT TCTATAGTAT
AGCAATCAAA GTAAGCTAGA AGGGTGTGG AATA

20_034 144
AGGC CTTGTTCTAA GTGCTAGACT GCAGTGGGGA GAAGTCACAA AATC
A/G
CTCCCCTTTT ATGTCTGTAT TCTAATATGG CAGAGGGGCA AGAGAGAGTG
AACATTGAAT TCAAGAATTA ATCCTACCTG CTACCCACCT CGACT

20_035 148
GGAT ATTCAAATG CCTTTTGTAT
GCTCATTACA AGTTTCCAAC TGTGTTCCAG CTAGAAGGTG TGAGGTAC
A/G
TGATAGCTGT ACTACTAAGG ATTTGCCATG AAGTACAGTG ATCTATAAAA
GAATATTCCA GACAAGCAGT TCCTT

20_036 147
A CAAAGCCACA
GGTGCAAGGG ATGCAGAGAG GGACAGGGCA CAGGAAAACCT GCTGGGAACT
A/G
GTATGCGAGG AGGAGGTGCT TACAGGACTG CACAGAATCT CAGGGCCCAG
TGCCAAAAAA ACCCACAAGA CCCCTTGTTT CAAAT

20_037 125
TTGGCCG CTGATCCAAC AAACCAACTG TAAAAGGAAT TTCTGAAACA
ATTCAAAGG TGTGACTACA GGTGACT
A/G
CTAGATAATT CCAAACATGT TCATCTTGTT AGAGGACTGA TAATGAACA

20_038 113
G AGACTGTTAC AGCCACTGTA GGAGTTTCAC CTCATTCTAT CCTTTCAACA
ACCCAAT
A/G
CGATAGATGC TATTATCCTC TTTAGGATAA AATCGAGGAA ACTGAGGTAC
AGTG

20_039 135
GGTGGATT TTCTTCAAAT
TCTAGAAAGT GAATTTCTAG TAAGTTCCCC TGGCACAGCA CCA
C/T
GGTAACTTCT CTGCAAAAGA CTCACCAAGC CATGGCCATG CCCTCCCAAC
TAGGTCTGGA TCAGCCCTGG GGA

20_040 125
GAA TCCTAAACTT CCTCATCAGC
GGTGGATTCA GTTATGGGCT CCAATGTTTC ACCCCTCCGT GAA
C/T
CCATGCCCTT ACTCTTGCAA CTTTGCAGTC CCTCCCGCTA AAGACAGAAT
GAACTCCT

20_041 135

Table III

CTTAG ACCAGATATG CCTCAATTC CTTTTCTAAG ATGGTGGCTG
TGGCCTCATA CACTTCACAG GGCTGTATAA ACTAAGCAC
C/T
AGTACGTGTG AAGTGCTAAA ACGGGTGTCC AGCACATAGT CACTGCTCAA

20_043 147
CAGAT
GGGGACAAAG AGTAACTCT ACATCTCTAA AATCTAACTC AACATCTTTT
TCTCAAACCT GACCCTTTCT CCAGATGTTT
C/T
TGTTTCTGCT TCATTTACAGC ATTCTTCCTT CCAGTCACGT GTGCTCAAAG
TGCCAAAGTT A

20_044 92
GTGAGTGTG GACAGTCATT TTGCTAATTC TTCTCATTGG TGGTTCC
A/G
CTAGATGGAT GATTTCCCTG AATTAGCCAT CATAACTGCC ATCTG

20_045 134
G CCATGCTTCC ACATGTGTGT ATGCTGTGTT TTCTCCTACT
TTCTGTTGTC ATCTTTGTGA AGACAGTGCC TACAACCCTC
C/T
CCTTCAAAG ACCTACATCT TTTATCTGTG TCTGTTGGTA TATTTCCATC
AA

20_046 114
GAGAGA GAGAGGGTGC GCATCCGAGT GAGCCAGTGT TAGCCAAGAA
GCAGGGAGCA GGGCTCGAAA GTCGC
C/T
GAGCGCCGAG TGCGAGGAGC TGTGATTGT TTTCTGGTTG AA

20_047 148
CT GAGGAAGGCC TGACCTGAAA CGATTTAACT TCTATGTGCA
CACTCTGAAT TAGTTTCTGG AACACCTGAA AATGCTCCAA AGGTCCCTCT
GGAG
A/G
CCTCCATGAA ATGTTGGTTA GTTAATGGAG TGGACCTAAT ATTAGCCAGT
C

20_048 146
TAGCAAGAG CTCCAGGCTC TCGGTCTTCT GCAGCAGGGC TGCCTCCTCC
GTCAAGTGCA GCATCTTTTA GGAAAGGAGT GTTCCTAGCC TGGCAGTG
C/T
AGTTAGGTAG AAATGAATGA GATGTCAGAA ACAATATTGA CTCTGAAT

20_049 147
GAAGCCTTT TGGGAACTCG GAAGCACTTA TCCTCAGACA TGTGGCTCAT
TCTTGTTTCC TCCAGGAGCC AATAGGTGGT AGCAACGGGC CAGCAAAGAA
A/G
CACCTGCTAA GGTGGGTGGT TCAGCCTAGC TGTCAAGGCG ATAGAAG

20_050 128
CCA AAATTAGTGG GAGCTGAGTA ATGACTGTGC CTTTAACTAN
GTCATGAAAT CACTGCCCTT TCTGGCTCCT TG
A/G
CACTAAGTCT GAGAATTAGT TCCATTTACT AGGCAATGAC ACTGTTGTTT
TC

Table III

20_051 96
GGCCCCCTTGG TCCTCCATCT AAATGTTGGA GTCTGACTGC CTGCAGC
A/G
CACATTGGGG TCACATTCCT ATGCCTTAGA GAGAGGAGAA GCTGGGTG

20_052 119
AGGG AAGCTGCACC CAGGGCTTCA CCCACAGGCA CCATCGCTTA
CTCTGCCTGG CTCG
C/T
GGGTCGGTGA AGGGAGTGGC TGCCCTTCTG CTCAGCTCGG TCTTTGTCCC
ATTATTTTCT

20_053 146
GAGAAAGCC ATCTAAACAG CTATTTCAAC ACAGCGTGGT GCAGGTCATC
ACACGACACT AAAAG
A/G
TGCAGACGCT AGTGCCGTGG CTCCAACCTT GGGGGTCTCC TGAGGCACAT
CTGGGGCTTT AACACCAATG CTGCACCCAT G

20_054 127
TTGCAGGAT AAGATTTTGG GTTTCGTTTT CAGCAATCTC AGCCTTGCGG
T/C
TACATGAGAT AAACATCAG AACAGACATA GATGCTTTCA AGTATTTTCA
GCAGAACTTG ACCTGAAATT TTGAATC

20_055 93
GAAG GGAGTCAGCG GAACTGGCTG GGGCCTGGCT CCTGCTTGGC ATTC
A/G
TGCCACGTGT GGCTTCCTCA GGTGGCCAGA CCACTCTGTC TGAG

20_056 136
TTGG TCATGAAGAC ATTTAATGGA TTCTCTGAAG TGGTGGCAAG
GTGGCAAG
A/G
AGAGTCCAAC CTGAAGCTGC AGAGCCTGGG ATTGCGCTGC ATGGAGAAGA
AAGGGTGTGC GTGATTCCAC GTCCTTTTC ATC

20_057 127
GCAAA GACCCCTCTG CACCGGCGAG CCAGCACCCC ACTGCCCCTG
TCCCCACGGG GCC
A/G
CCAGCCTGGC CGCCTGAGCA CAGTGCCTTC CACTCAATCC CAGCATCCCC
GGCTGGGCCA ATCAGCCT

20_059 147
C TCTCTCTCTC ATGCATGCTC ACTTTCTTCA ATGAGTTGTT GCACATTTAT TGAGCATCTA
CTATGTGCTG GCACTGTGCT AGGGACATAG ATAAC
C/T
AAGGCAGGGC TCCTTTACAC CAGGCCTTGT TAGCTAGGAA AAGGGACCAG

20_060 110
TGATGCCTT CATGCTGCAT CTTTTGGAAG GGAGGAGCAT TGTGTCCTCA
CAGAGCAGAA AAT
A/G
GAAGGGCCAC AGGACAACT CCCTCTATCA AGCCTTTTCA TAAGGGC

20_061 132
 CATCG CATTGCCGGT GCACTCACAC ATACCCACAG TTA CT CAGAC
 TGGGACCACA CAGACATGTC AATCGACCTC ACATGC
 A/G
 CAGCCTTGGG AAGTGAGAGG AA ACTGGAGC ATCCAGAGAA TATCCATGCA

20_062 125
 ACACCATT TCCCACACCA GCTTACACCC CTGGCACGTG CACCCAGAGC
 CCCCAGTTCT TCATCAGGCC AGTCATCGTG
 A/G
 TCATTGTTAT CTACTAACAT CACCTGAATT TCTCAGGAGC TTA CTG

20_063 143
 CACTGC ACCCAGCCGG TTATGCGATT TTTATCAGAC CTTAGATATC
 TCTTATATAG ACAGGCAGAT TATGTAGTTA CAGACAGTAC CTCAGAAGTT
 C/T
 GATGTCTGTG ATCAGTTTGT CTTTCGAAAT CTTGCTCACG AATGAG

20_064 125
 TGGAAG GCTCTTAGGA CTGCTTGAGT GTCTTCACAA CATGGTAGCT
 G/A
 GCTTCCTTGA GAACAAGTGA TCCAAGACAG CCAGCAGCAT CTTTGGATTG
 ATTTTCTTGT CAGCAGTGGG GTGTAGTG

20_065 145
 CAA GAACACAGCT TCAAAAAGGT CGCACATAGA GTGGTCAAGG
 AGGAAGGGGA CACC
 C/T
 GCCTACCCAG CCAGATCAGC CGAATCAACC CTGGTGATCA ATGGGGTGAC
 AGATGTCGCA GCTAGATCGT CCTCACATCC AAAATAA

20_066 130
 ACATTC CCAATGACCA TATAATAGAG AAGGAGAAAC AGTTTCTACA
 TTCCCATATG GTATCTTAAA GATTTAAC
 A/G
 TTTCAAAGAT CAAGAAAGTT TACTTTCTTT CAGATTAAAT AATGAGAAAG
 GCAGC

20_067 129
 AGGCTG CAGATGAAGA GATGCATAGG GTGAGGTATG GGAAGGGGTG
 CAGAGCTTCT GCGTCCTCCC TGGGCCT
 A/G
 CCACCTTCTA GGAACCCAG CATGTCTGGC TATCAGGAAG CTCTC

20_068 142
 CAGACAC CTCAGGGCTG CATTAAATTGG AGGGACGGCT CTTGTTATAG A
 C/T
 GAGGAAGTCT GAGATGTCGT GCCATACATT GCTGTCCTCA TAGAGGTAGG
 TCATGGAGGA CTGCAGCGAG GGCTGCAGGG TGGATCGGTG ATAC

20_069 105
 GCCGCGTG TCATGAAATT CGAACAAGAA GTACTGAATT GAAGTGGGGA
 TGAGAGGT
 C/T
 AGATGTGAAG GGCTCCTGCC AGCTTACCCA GGTCTCTTGC TCAGAAGA

20_070 116

Table III

CAGAAGCAG GAGCTCAGGG CAGATAGAGG CCTGGAGTGG GCTCTGCATA TGTTC
 A/G
 GAGGTGAGGA TGCAACAGGA GAGTGTCTG CTGTCAGGAT TAGAACCCCA
 AGAAAGGGGT

20_071 103
 TTGGGATCTG GTTGGTGGTC TCAGGGATAA AGAGGTCAGG AGTCATCCAT T
 C/T
 CTGATTGCTT CCTGTCTCAG CCTCACATCC AGCCCAACAG AAAGCCCTGT
 T

20_072 128
 GGGGA AAGAAGGCCA GGACACGCAG CCTGGCATCA CCGTGCCACA
 T/C
 GATGTCCCCA CTCCAGACAA CACAGAGGCT GCCTGGCCCT GGAGACTCAC
 CACGTCTGCTG TCCTCTGGTT GGAATAATG AG

20_073 123
 CG AGGTCCGTGC GTTGCCGCTC GGCCGCCATG TAAAAGTGGG TCAGCT
 C/T
 AGCCTGGAAG GCCCGCTGGG TAGAGGCAAA GGCTGCCAGC TCTGGGAAC
 CTGCACGTTG TGCCTCCCCA GCCCCT

20_074 120
 A CACCCTGCTG CAGACTGGCT TCCCCTGCCG TGGGTGAGGC AGGACAGGGG
 CACACCAG
 C/T
 GGGAGGGCTG AGAACTCTTT ATGACAACCT TCCATCTAGA GAGAACTCTT
 TTAATTGCCA

20_075 108
 G AGATCAGATT AATGCCATGA TTACTGCTCT GTGCACCTTG TATGTCCTCA AAGAGATGA
 C/T
 CCCACATTTG TGTGAATGTC CAATCTGATG TGTGAGCCGT CTTTGAC

20_076 116
 GTTCCACTG CAGAGACGAA TCGGTTCATT CACAATGATG AACTCATCCT
 CTACTGACGA ACA
 C/T
 CTGAACTCTT TCCTGTGTTT TGCTATTATA ATTAGTGTTG CAACGCATGG
 CCT

20_077 131
 TGGGAGGAA ATGTTTATAA AGCATATATT TGATGAAAGA TTTGTATTCA
 GATTACATAA AGAACTCTCA G
 G/A
 ACTCAATAAT AGCCTTTCCT TTTGGTGGTG CACAGCAGCA ATATGGTGGT
 GAAAATTTCT

20_078 115
 GGACCTTGGG TGCAGATCAA AACTAAGCT CCATGTCCAG CCAGGTAGGC
 CCCACACTC
 C/T
 ATTCTTAGAG CAGAAGAACT AATTCCAGCT CTACCTTCCA TGGCTGGAGT
 CTGCT

20_079 109

Table III

GGCCATGGCA TGTGTTTACA AAGTTATTTT GGAGATAAAG TGAGACAATG A
A/G
CAGAAAAGGC CGAATGCAGT GCTCACCCAC TATTTTTTTT TCTCCAAACA
TAAGCAT

20_080 137
GGATCTAGA ACAGCCCCTA GTCCCACCGC AGAGTGGACT TGGT
C/T
TCCTGGCCAA TTGCAGGCAA TGAAACTCTT CCTTCTTCAT CCTTTCTACA
TGTGGAATCA AACCTAGAAA TACCCTTAGG AAGGAGTGGA TGA

20_081 111
TAAC CCTAAACTGA ATCCTCTCTA GAGTACAGTA TATCCCAGGG
CTCACTTGGG GTTCTGTTT
C/T
CATCTCTCCA GAGCATTATC TCAAACCTAC CCAGACTCGC CCACTAT

20_082 101
CATTTG GTAGATGGGT CTGTAGCTGC TTTGGAGAGG GCACCC
A/G
CAAGCCAAAT AGAGAAGGGA TAGGGTGCTT GCCAGGCTGT CCCCTAGAAG
GAAAAGGT

20_083 131
TCCCAGGCTT GTAAATACGT GGGCCCCTGA ATTATCTGTT GTGAGGCTGT
TATCTAGAAG CAGGGGTTTG GGGTTTGAAG CTAGG
A/G

TCGAGAACCA TCAGAATACA AAGTACTGGA GAAAGAACAT TCCAG

20_084 133
CATCC TTCAGTACT GACTGATAGT AGAGGGAGAG TGACCAACTG
GCTTGCCACT TGCTCAGTCT GCCCAGGACT GA
C/T
GGGTTGCCCC GTACGTGGGA CTTTCAGTGC TAAAACCACT AATGTTCTGG
GAAAA

20_085 143
TGG TCTCATGTCT CCGAATAAG TACTCAATAG CCACAGCTGA
GGTGCCCTCAT G
C/T
ATCATGGGCA GCCACAGCCC CTGCCCCAGT CCCCTTGTCT GATGAACACA
CATCATGATG CCACTCTATA AAGAGGACCG TTGCCAGA

20_087 127
TGGCCCTGAG AGTTGGAAC GAAGCCCATG TATAAAGACT GG
A/G
GGGCCGGGTG TGGTGGCTCA CACCTGTAAT CCCAGCACTT TGAGATGCTG
AGGTGGGAAG ATAGCTTGAG CCA

20_088 137
T CTTGGCCTTG CTTGAGATTC TAACTGGAAC ATGGAGACGA
TGTGTATATA GGGAGGGA
A/G
GAGAAAAGCA TGAGTGGCTC TCTCACCCAC TGATTGCTAT ATTTGATCCT
CACTTAGTCT TGGGAGATGG AGCTCCT

Table III

20_089 141
 TGGT AGCCAGTGCA TGGTGAGCCT GTTTCACCAC TTTATTAGTC
 TGTTTTTCATA CTGCTGATAA AGACA
 C/T
 AGCCAAGACT GGGCAATTTA CAAAGGAAAG AGATTTAATT GGAATAACAG
 TTCCACGTGG CTGGAGAAAC C

20_090 149
 CCACTGTT CCCATATTCT CGTTATATTC CACAATGACA CATGGCCTCT
 TAGTTTTATT TCCATTTCTG TGGTCTACCT CAATAACAGT AT
 C/T
 GTTGTGGAAT GTTGAAAACA TTGTCACCTC CTTGTCAGAC CATTTTGGTG
 CCATAAAT

20_091 118
 G AGATCAGACC TAACCAACTC TATCTTGCCT CTACCCTTTA AGCTGTCCTT
 GTTCATTCCCT GGGTGTA
 A/G
 GCAGAATAA CCTTAGGAAG GAATTTAGTT TATGGTTTGA CTGAAACAA

20_092 134
 GTC TGGTACAGTT TTCCAGAGGT TACATGATGT GTGATGATAT
 CATCACTCTG ATAGCTAATG GAAAGTATGA
 T/C
 TGTATATTCT GTAATGTTCC AGGAGTTTCT GAGGTTTAGG TTTAGGTTAT
 AAAAGGGGGC

20_093 138
 TCCACA AAAAATGGGA AGACTCCCCA TTAGGGAGCC TGATGAGGGG
 TCTGTGAGCT GGTGCTGAGC CTGGAATGGG G
 A/G
 ATGCCATGGG TTGAGTTGTG TCCCCCTAAA ATTCATATGT TGAATTCCTG
 AAGTAGTTGT

20_094 133
 AGTGCTG CAGTGAGCAG GCTTATCCAG CCATCTTTGC ACACATGAAT
 GTTTCTGAGG ACATCTTTCT AC
 A/G
 GGTGATATTG CTGGGTTGTA GGTGACAAGC ACTTTGAAAC TCGACTCCTC
 AGCCAAACTA CCC

20_096 131
 C GAAACTAAAC TTCACATGGA GCTCCCAAAG ATTTTCATAA
 TCTGACTATT AATTTTCATT TC
 A/G
 ACCACCATCT TTCTAATTCT ATGTGTGTAT CTTATTTATA TGTCAGTTGC
 TTGATAGTCT AGACCCT

20_097 149
 ATCTCCAT CCGAGCATA ATTAATAATA CCTGAATCAG ATGTTTGATG
 TGAAGACTGT ATTACTTTAT GAATGATGTT TCCCAAACAG TGGCA
 C/T
 ATAGAAGGCA TCTTTATGTG TATTTTAGGA GCATTAGCTT ACAAAGCGGG
 GAGCC

20_098 127
 TGATGA GGAATACAT TCATTCAACA AATATCTATT GAGTGCCTCT

Table III

TTCACACCAG CTACCGGGCT AGGTAGCTGA ATG

C/T

TTGTCTGAAT GTTTGTGGTC TGAATGTTTG TGTTCTGCA AACTCA

20_099 125

CCAG GGCCTGGACC CCGTTACCCT ACAGACCTCA CTACCCAGCC
CTCCCTCTCA CTCACTGCTC CAGCCCCATC AGCTTC

C/T

TTCTGCTCTT CCAATGCGCC AGACACGGTC CCACTTCAGG GCCTC

20_101 120

CTGG ATGGAGTTGA GTCAAACCTGC CTCTGGCCGC CTCCAGCTTC
CTGCTGGGCT TTGCT

A/G

TTAGGGGCAC CAAAGAAGAT CAGAGGGTCG GAGAGAAAGG GTTTGCAAAT
TTGCAAATAT

20_102 106

TCTGAGCAAC TGGACTATCT TTCCAGAGTC CAGGGATTCC AGGTAA

C/T

TGTCTGGCCT GAGCTGTGAT GGCTGTGCCT CAGGACAGTC ATCTTTTGGC
TTCTCTCAG

20_103 126

GC CGTTGTTTAT CGCCCTCCCG TGGATTAATC CCCTGTCAGT
TAGGCCAGAG AAGCTCTGGA GAAGGCCTGC

A/G

TAGCATCCCA TGTGTCAAGG CCCCCTTTGA TACACTTTAT CTGCCCTTAT
CCC

20_104 148

CACATG GCACAGAAGT GCTTATAGTT AGGAAACAAA GGCTGGAATT
TCTTTATGCT CTGACA

A/G

CCAGGAGGTG CTGCCCAAGA CTCTGAAATG ATTCCTGAGC CAGCCCCCAG
GCCCTGCAG TAGAGTTTGA GTCTAAACCA AAGTG

20_105 120

CTTGCCCTG CCCCCACCAC CTTATGTCTG TGCCTCCAAC ACATCAGGC

A/G

TGGTCCTCCG GGCCTTTGCA TGGGCTGTTT CTTCCACTTT GCCCAAATGT
CGCTTTCTCA GGGAGGCCT

20_106 124

CCACTCTC AAACAGAAAG TTCGGAAGGG AGGCAGGTAA GTGTTAGAAA
GGCGTTAATG TCATGTT

C/T

CTATCAAACCT GAGACTGCCG CCTAGATGCC ATCAGAATGA TTGACAGAGA
ATGAAATG

20_107 147

CCCTTC TCAGAGGGCT ATGTAAACAT TTAAAAAGTT ACTGTAGTAA
GTTGCTTGGA GGAGTGCCTC ACCCATGCAC TCAATAC

C/T

ACATTCGACA AAGTGATACT GAGGCTTTTC TGTGCCAGGA ACGAGGATAA
AGATGGTGAA AAA

Table III

20_109 111
 GGAGT TCCTTTGTGT GAACCTAAAG GATTGATTGA GATGATAAAA T
 A/G
 TCATCGCTGC TCTGACTACG TCTTTGATAT TTGTATGGAA TAATTACATG
 AATAGGTCCA ATGG

20_110 128
 AGTGCA CGGATTCTAT TAGGGAAATG CGGTGGTAAT TAATGAATCC
 TGCCAGTAAT
 C/T
 GGGAAAGGTGT GAGTCCCCGT AATATCGTAA TGATAGTCAT CTGTCTGCGA
 ACCCCCCATC ACTCTGAGAG A

20_114 137
 CCAAT TTAATTACTT CTTGCTTCTT CTATTATAAG ACACTTATTT
 CCTGGACTGA GAGCCATCTT CAACTCTATC AGCTACTACT
 A/G
 GCTTTTCTCA AGTGACCCAT TCAGCTGTCT CTTCTACCCA CAGTAATGCT
 C

20_115 143
 AGGTGG CACCTGGCTG TGATCACTGA AAGCACTCTC ACCAGCTGGG
 CTTTCAGCCA AGGTCAGGAC TTTGCACCAC CC
 C/T
 TTCACACATG CCCCAGGCC ATGTCCCAGC AATGCCCTCA GGACCACTGT
 AAAGGAAGCA CAGTG

20_116 139
 TGA TTCTGAAGTG CTGTGAGGGT CTGAACAGTG GCTGAGGTTT
 ATTTTATAGA ATTTATACGC CTTAAAG
 A/G
 CTGAACTCAG AAATTTGGGA TTCCATTCCC ACATGGCCAT CTAATACAGG
 TATGATCTTG AGAGGTCA

20_118 128
 CTGGA TGACTTTTTG GCACCGCCTT AAATTCTGTG GCTGAGGCAA
 GTACCTCC
 C/T
 TCGTCATACC CTAATCCTGA CTCTGCACTA AGTACTCAGC ACCCTACAGC
 GATTGAGGCC ATTGCTGTTG TTTT

20_119 125
 GCCCACATGG TGATGCGTGC AGTTAAACAG GAAGCTGGCG GAATGAGTGC
 CTGCGTGGGG A

C/T
 GGAACAGTTC CGCGTCTCGA GTACAGTGGT GGGGAGATGT GTCTGTGTGT
 GTGATAAAGC TTC

20_120 136
 GATCATG AAAAGTTTTA AGGAACTCA GAGAAAAAGA GAACAACGCA
 GCTTAAACT TTTAAATGT CCTCCCTCAC CCGTGGCTCA
 G/A
 ACAGCCCTGC ATCTGCCGTG GCCGGCACGT TTCTGGTTGA ACTGCCTT

20_122 128
 T AAATACAGCC GGAATGATCA ATACACGTGT CCTAAGATCT

Table III

AAGGAGAAGA GCTGTAAGTC ATAA

C/T

GTATGTCCTC AGTGTGGTGC TCCCTCTCCC ATGTTCAATA CTGAGTGTA
ACTTTTTTTC CA

20_123 101

ATGAGCA CTCTGCCTTG GTCCCTGGAA GCCTTCCCTG CCATGAGGTT
GGAGTCAC

A/G

TGGTTCTTCG GTGGGACCCT TAGAATTAGG ATTTAGTGAG CCCAG

20_124 119

TGTCC ATCATCTCAG AAAGTGCTAC TGGGTAGTAC CGAGGGTCAG GGTG

A/G

CTGCACATCT ACTTTGCTGT GAAACAAGGG CAGATGTAGT TTGGATTGGC
TAGCCTTCCA GAGTTCTCC

20_125 147

CTCAAGCGG TCCTCCCTTT TCGGCCTCCC AAAATTCTGG

GATTA

C/T

AGGCGTAAGT CACCATGTTC ATCCAAGAAA TAAATTTTGT GTTGTTTATT
TGGACTAAGA TATCATCTTA TTTTATCCTA TGAAGGATCT GTTGTAAGCT TC

20_128 120

AGCGGAGCTG TGGAGAAAGG GCGCAGTGAG CAGAGGGGAC TTGGGCGGT

A/G

AGAATGAAAG AGGGGACGAG GGAGGTTGGG GGTATATGAA TGGAAAAGAG
TAACGTCGGG GGCAGGACAA

20_129 101

AA CCACTCTCTC TCCTCTCAAG GGTAGCTCAA GCACTCTCTC
TTTTCATCAC TCATCT

C/T

GTCTTACTTC ACTACCACTA GTGTTCTAT CTACCTGGAC TC

20_130 146

CC GGAAAGCTTT GGGCAGCTTG AACAGCTTCC TCCCACCACT
CTGCACTCCC TGAGCCCAGC AGCCTGCTTC CTGTGAACTT TCTAGAGCAA
ACGGCCCC

C/T

GTGCAGAAGC AGCATCCACG GCTGAGCAAA CAGGTGGTCA CATGG

20_131 143

GGCCACAGG CAGTACTGAT AACGCCAAGG TTGCAGTCAG CTAACATCCA
TTCTCCTATC AGCCAAGGGT CTGGC

A/G

ATAGCCGGGC ACAGGAAGAT TGTGAGTTAT TTCTTCAGGA GGGCTGTGTG
TCCTGGACAG TGAAGAAG

20_132 143

CATCAGC CAGGATTGCC GTTACAGTCT TTTTCTCAGG AGCTACAAAG
ATCTCTTCTT GTTACTAAAT

G/A

GTCGCACCCC AGCAGCCTCT CTCGCACACC GGGGCCCTGC ATGTCAGATG
GCGTGGTCTG CAGGGGGAGC TCTGT

Table III

22_001 127
 AT GCAGATGAAG CCTTCAGGTA GCAGGCTTCC AAGATAACAG
 GTTGTAATA GTTCTTATCA GACTTAAGTT CTGTGGAGAC
 A/G
 TAAAATGAGG CATATCTGAC CTCCACTTCC AAAAACATCT GAGA

22_003 147
 TCT TTCAAAAATG GAAGGGAAAT AAAGACTTTC TCATGTGCAC
 AAAAGCTGAA AGAGTTCATC
 G/A
 CCACTATACC TGCCTTATAA GAAATGCTAA AGGGAGTCCA TCATGTTGAA
 ATAAAGAAT GCTAGGCAGC AACATCAAAA CAT

22_004 148
 CC CTCCTCCTGC TTGGCTCTGT AGCTGTCATT GTCCAAGCTT GGAGGGCTC
 A/G
 TGTACAAGCT AACATGGAGG AGGAGCTGGA AGATTGCCTC TCCCGGGGGT
 CTTGCCTGTT CAGTGGAAAG AAGATGGGAT CATTACAGCC ACTCCA

22_005 147
 A CACTCACCT TGCTCTGCTA ATAAGAGGAA GTAGGCGGGG
 ACGTGGTCAT CACCCTGAGG
 T/C
 CCCCACCCA GCTCCTCACA GTGGGAATAA ATGAGCACAG CTCTACAGTG
 GAGCCAGCAG TCTCGTGACA AGTCTGACAG CAAAG

22_006 149
 TC AAGTGTCCCA CCTGCCTTGG CCTCTGAAAG TGCTGGGATT
 ACAGGCGTGA
 A/G
 CCACCATGCC TGCTGGTCTC TGCTTTTTGA ATGCTGACAT GCTGACCTTA
 GATGTGGGGT AGGGATGATC AGACCAAGTA TTCTGAATTA TGGACT

22_007 140
 AGCCG GTTGACTTCC
 TAGGGCCTTG AGTCACATAC CACCACTCCA GCGCTGGGTG ACTGC
 A/G
 GGTGGGTCAT CATGCAGCCT CATTATTCC CCTCACTGGC CTCCAAGGGC
 TGCTTTGAGA AACCCTCAC GCAGCACAG

22_008 143
 CCCCC AGGCTGACTC AGAGACGTGT CCCTCCACCC GTGTGGCCAT
 GTGTTGTTCC ATCCTAAAGC TATGGCACAC TCCCATCAT
 A/G
 TCCCTCAGTG CAAACCCACC GAGCCCTGTG GTAGGGACGC AGTGTCTAGG
 AAGGCCTC

22_015 110
 T TGGAACCTTA TTACACTTCG AGTCACTGGT TTGCCTGTAT TGTGAAACCA
 A/G
 CTGGATCCTG AGATCCCCAA GACAGAAATC ATGATGAGTA TGTTTTTGGC
 CCATGACA

22_016 149
 CCAAATGT CAGGGTCCTG GCACCACAAG GCCTTCCAAG AATAGGAGCC
 CAGAAGTCCT CATG
 C/T
 GCAGTTATAG CAGGTGGAAT TCTACTTTTT TATTGAGGTA CAACTAGCAT

Table III

ACAGTAAAGT GCATAAATCT TAAGTGCATA GCTTG

22_018 129
TC ACTGATGGTC ATGCTGGTCT CTTGTTTGTG GAGCAGCAAC
ATAAAGAAAT TGTACAGTG AAGAAACAG
C/T
CACTTTTGGT CAGCCAGGGC AGATGGAAAA AGGGCCTAAC GGGTACACAA
CGTGAAC

22_019 132
TCACAGGACG TCTCCTTCAC AGTGGGTCTG TGCTTCTTTG TGGCCCAGAA
CAAATTAGTG GGGCTTGGAT TTATGAG
A/G
CAGATTCCCC AACCTCTGGA AGGTGTGACT TGCCACAGGG AAAGAAGGCC
CCTC

22_020 141
TCAAGTGA TCCTCCTGCC TCAACCTCCC AAAGTGCTGG GATTACAGGC
ATGA
A/G
CCAGTGCACT TGACCTGATA ATAGGATTCT TTACACTTTA TTATCAGAGT
GATCTTGAAC CCTTCTGGAA TTGCATAATG TCAGCCCC

22_021 144
GAACT CCAAACCTCCT TTCTATTCTT TGTCAGGCAG AAAGCGATTG
G/A
CCTGGGCTGG TTAGCCTGGT TCTCATCTCC ATGCTCAAAA GCTATGTCAG
GCTCCTGGGA AGGGATGCTA TTGATACCTG GCTACTTGCC TAGCTGCT

22_023 132
GTGC AGGGCAGAGT CTCAACACAG GAATTGGAAC ATAACAAATC
T/C
GCCGACTGCC AGCTTTGATC TCACAAGGAT GGAGTTGGGG AGGTGAAGAG
AAAGTAAATG CTCTCTCGAC TTTCCAAAGG AAAACAA

22_024 124
GGAGAGGGA TGCGGCAAGA GTTAGGAAGT GTCTAGATCC TTGGTTCATT
TATCAACAAA TGTGAGCCAA ACCA
C/T
GTGGTGGGTG CTAGAATACA CCAGCGATAA GAACTGGGAG AACACTGCCT

22_025 106
CAATC TTTTCTTTTC TTTCAACAAT CTGTTTCATGC CACAACACT GACTA
C/T
ATATCTAGCA CGTATAGGTA CTGTGCTAGA AAGAGAAGCT GGAAGGTGGG
AATAC

22_026 102
TATGTGGT AGGGTGTTAC GTTGGTCAGT TTTTAAGGAT AGTCTACAAG
ACCATACG
A/G
TCTAATGGAA AGAGAGAGCT AGACTGAGAG GTATAATGGC ATTC

22_027 127
GA GCTGTTTGCT ATGGTGGCAG TAGCTGGAGA GCTACTGTTA
ATTAATTTGA GCAACAGTGC
A/G

Table III

GCTGATAAAT TTGATCTAGC AGGGAGGTCT GGGACTGCCA TCCTGAACTC
AAGGTTCTCA AATC

22_028 120
AGTAAGGG TAACTTGTCA CTCCTTCACC TACCATGTAA TCCTCATGGG
CAA
C/T
TGTCACCCAT TTCACCAGGC GAGAGACAAC CTTGGCAGGG AAGAGGTACT
GGCAATCACT GGTAAC TG

22_029 127
C GGGGTTTCTC CATGTTGGTC AGGCTGGTCT CAGGTGATAC GCCC
A/G
CCTTGCCAC CCGGAGTGCT TGGATTTATA GCGGTGAGCC ACAGCTCCTG
GCCTAGATTA TAGGTTTAA CATGTGACCC C

22_030 110
TGG CTGAGTTAGA
GTGGTGTAGC ATTGAGCTGC TCAGTTCGTG GCAAGGGTGG GATCACGGCT
A/G
AGGCTGCAGA CAGCACCACA GTCTCCCGCT GCGAGGGTCG GTTGGT

22_031 105
CT GCCTCTTCCC AAGACTCAGC CACACAAGAC TACTTCCTTC AGGAGA
C/T
GTTGGTTTAT GTGCTTAGGG TCTCTGCATG AGAAGTTCCC TGCTTGGGAC
GTCCCT

22_032 124
CA TGGCAGAAAT CAGCAGCTTC CCCTGGGGAT TGTCTACTGA
GCACCTACAG AACCATATGG G
C/T
CTACCAGGAC TGGGACAGTG GCCCAAACA TAGAGGTTCC TGATCGGCTC
AGGAAC TAGG

22_033 128
CT GGAGATAAAG CCTCAGATT TATGACTTAC ATGTGATGAC TGAATGTTCA
T/C
GTCCCCATTT GTGTTTCCTA GGGCTGTTAT CACAGATCAC AGCTACAGTA
AATGTTTACA GCAATTCTGC TGTCC

22_034 121
TTAG TATGTCTCCT TCCATCTCAG GCTGTGACAA CCAAAATGT
CTTCAGACAT TGCCA
A/G
ATGTCCCTAG CTGAGAATCA CTAGTTGAGA ACCACTGCTT TAGAATGTAA
GCGCCTTGAG G

22_036 124
TGA TGGGGTGTTT GGAGTTGACA AAGTATCGTA AACACTCATG
TTAGCGCCTT TGATCTCCA
C/T
GAAAGCCTTA AAAGACGGGC AGGATTTCTT CCTTTTTTAT AGGTGAGCAA
ACAAGGGCAA

22_037 136
CA AGATGTAGAG GCACGTGCTT AGGGTCACCC AGCTCAGGCC TGGTAGGAGC

Table III

AGAACC

A/G

GAACCCAGGC CTGCTTCTTT GTTTTATTCA AATCCTATGC ACAACTCAGA
CAGTTCTACA ATGAATTCAA GCCTGAA

22_038

124

AG CACCGCAATA CTGACAGTCA ATCTGGTAAT GGATTTGGCT
GCAAAGTGAC TAACTCAGGT AGCATGTACA G
C/T
ATGGATCTAC GGGACAAATG GGATGATCCA CATTCCAGGG TGGACAGAGT

22_039

141

TGGA GAATTGGGGA CCTTTTAACA ATTTTCTACA AGAACAGTGC CGC
C/T
GGTGTGTTG CAGAAGAGAG CTTAGACTTC ATCTATGAAG CCACAGAGCA
TGGTGTGGAA ATCTGCAGTT AGAAGATGGA TTTTGTGCGA CAG

22_040

147

TTTG GGAAGTGTG CCAAGCGGG AGGAAGGGTA TGGAGCAGAT
CCATGGTGAT CACTGATGCC ACTTTACTCC CTTTCCATTC CC
A/G
GAGGAGAGAA ACCATTTTGG AGCTATAGTG ACCTCATTTT ATGGAAAATA
ATATTTGGCC

22_041

148

CAGCCCTGA CTGCAACCTC TCTGACCACA GCTCAGAGAG GGCATGTGGC
ATGCTCACAA ACAGTCTGTT AGGGGCTTCC
C/T
CTGGGTCAGA ACTCAGACCC CTCGGCTCTT AGTCCAATGC TCCTCTCCTA
ACCCAGGTTG CCTTTGGG

22_042

128

CCC AAATAACCCT ATGAAATAGT TATTATTATT TACATTTACA
GGTGAGAAA CTGAAGGCTA CAGAATTAAA AGACA
C/T
GAAAACAAAG CTCAAAGAGT GAAATGACTT GCCCAAGGGC ATGGGAAGC

22_043

111

AGGGCTTTG CCACCTGGTT GAGGAGACAG ATACTTGAAA ACAGAGAAGC
ACAAG
A/G
AAGTGTCTGG ATCTTTGCCG ACATCTGAAC TGGCAGAGGC TGCAAATGTC
TGAGGG

22_044

126

GGGGGGA GGCAGCCATG CTCTGAGCAC CTGCTCCTCA CCAGGCATT
C/T
ACCAGGCACC ATCTCACTTA ATCCTTCCAA GAATCCTAGG CATTACGGGA
CTTCCATTG AGGCTCAGAG AGGTCCAGT

22_045

147

TCCTGAGCC AACTTTAAAC ATCTTAAAAG CACTATCACT ATTCCCACTT
TGCAGATGAG GAAACTGAGG CCTCACAAC GCTAC
A/G
CAGTGGCTTC CAGCCTCCAC GGCCCCAGGC TCCGTTCAAG AGCTGCTGTG
GGATCCTGTT TC

22_046 110
 TTTTA AGTCCCTACA TTTGGGTTA ATTTATTACG CAGTGATAGA
 TAACTAATAT ACCTTGCCAA
 G/A
 CAATTGTTAT TGGAAGGCTG GTAGACGGAA TAATATTCCT GAAG

22_047 144
 AGGTGTGCAC TGTCACCCTC AAGCGGCCTG AGAAGAGGTG GTGCAGCCAG
 CAGGGGCCAG TCCTG
 C/T
 GTTCTTATCC CCCTCTTGTC ACAGATGCCT GCAGAGTGGC TGGTGATGGG
 GCCTGCGCTT GCTTGCTAAC CAGTCTCT

22_048 104
 TGGAAGGC ACAGTCCAGT GAACAGACAG CCATGTGAAC AAA
 C/T
 AGATATAGAA TAATTCATTC TACCAATGCT ATGGTAGAGG TGTGGGCAAG
 ATTCTGGCTC TT

22_050 133
 CCCTGC CACTTACTTG CCATATGACT TTGGGCAAAG GACTGAACCC C
 C/T
 GCTGAGCACC AGCTTCCTCA CTTATAAAAT GGAGATTAGG ATATTATGGC
 AATAGTACCT ACCACATAGG ATTATTTTGA GAACT

22_051 128
 TTTCCATT TCAATTATCC CTTTCTAAAA CTGGGTCTTA AGCAAACCTGG AATTG
 A/G
 GTGTTTCCCA GGTCTCTTCA AACACTTTAA TATGTTGGTT CCCAGACTTC
 GGTTTCAGGG AACTGTAAGG TTGA

22_052 132
 T GAATTATAGA CTTGAACCCT GGACTCTCAC ATTAAAATC TGATGCT
 C/T
 GACCAACTGA GCTACACAGA CTTCTAACCA GACTTTTTAT CCCTTTCACA
 GCAGCATCCC CACATCCCAT GAGTTAATTC TGT

22_057 149
 CATGACA GAGACCAGCT CTTGTTCAGT GCCCCCTACC TGCTGGCTGC
 TTCCTCGGCT CCTCGAACAG ATCAGCCGAG CTTATGGAGG AACTTGC
 C/T
 GACAGCCTCT CTAGGCGGGC CCTGGTCTCA TACTAGAGAA GACAAGGAAA
 AGGA

22_059 143
 GGTGGCC CAGCGGGGCA AGAGAGTAAG GACTGGGAGC GAGTGGGACC
 A/G
 AGACAAGAGG CCTGGTCCCG CCTTCCTTGA GAGCAGGGCA GGGTGGAACC
 CAGCCTCGCT CCTCCTCAGG GGCTGGAATG GAAGCCAGAG AACAG

22_060 135
 GAAGCAG CCCCAGCATC AGGGACAGGC CAGGAGTGCA GAATGCATGG
 AAGCTGGTCA GGTCGGAGCC
 C/T
 GGGATGAAGG AAGCACAGAG ATGCAAGGGT GCCAGGGCCC ATGGAACCAA
 GAGCCGATGA TCAAGGC

22_062 144

Table III

CTT GCCACATTGC TTGGATGGCC TTTCACCAGG TCTGATCCGA GGGTGGTCTC
 G/A
 TCTTTGTCTT AGCAGCCGAG GTCTGTGACC TTGACCACCT GGTGAAGTGT
 TTGCTGTAAA GTCACTCTTT TTTCCTTGCT TCCCATACTG

22_064 112
 AGT GGTGTGATCA TAGCTCACTG CAGCCTCGTC CTCCTGAGCT
 CAGCTGATCC TCCAGCCTCA
 G/A
 CCTCCTGAGT GGCTGAGACT ATATGTGTAC ACCAGCATGC CTGGCTAA

22_065 112
 GACTGG GATGGGCAAG AGGTACGGGA CCTGCTCGGC TCACCTCCCT
 C/T
 CTGCAGAGAG ACTCCCAAGG GCTCAGCTGC TCAGAACACT CTAGTTGCC
 GTGAGGAGCC CAGGG

22_066 138
 TGCAAAGAC ACAATAAGCT ACGTATACAT AGTGGTATAC ATATGCACGC
 ACATACATGC AC
 A/G
 TCCACAATCC ATGTTCTAT GCACCTGTTT CTGCCCATGC AGGTTTCATGC
 ACACATATTC CCTGCAAATG TTTGTC

22_067 147
 GTGAATGGAG ATGGACACAT AGCCCTGGGG TAGTTGGAGC TTTTCCTGGC
 A/G
 GTATCCATGG CAACAGGAAG CACAAACAGA AGCATCATTC TACAGCCAAC
 AAAGAGTTCG TTTTAAAAAT CACCATTATC TTTTCAGAGT GCTTCT

22_068 135
 AAGGGCTGAG AGAACTAGAA GAGCCTGATA AGGATCTGGA GAAGAGGCAG
 CTTCCGACCT TTGATGCCAC AGTCACTCTG
 C/T
 GCTACACCTT CATGCAGGGT CCATGCTGTG GCTGATTTCA CAGAGTGGGA
 TATT

22_069 145
 TGGCTCAGTT GCCTGCTTGA GGGGATATTT GTGTCTGTCC CTCATACC
 A/G
 GCCACACAAA CCTCCTCAGC CTGGACCACA TGCACGGGTG ACTCCTAGAT
 CCCTATCTTT GACCTCCATG CCTAGGCACC TGGCATCTTC CAGCAT

Claims

What is claimed is:

1. A method for designing a multiplicity of primers for simultaneous
5 amplification of a multiplicity of target DNA fragments in a single multiplex polymerase
chain reaction comprising the steps of:
 - a. aligning a first primer and a second primer; and
 - b. selecting the first primer wherein 1) the first primer at its 3' end does not contain
four or more bases that are perfectly matching to the 3' end sequence of the first primer or a
10 second primer; the first primer at its 3' end does not contain seven or more bases that are
perfectly matching except one mismatch to the 3' end sequence of the first primer or the
second primer; the first primer at its 3' end does not contain six or more bases that are
perfectly matching to a sequence anywhere of the first primer or the second primer; and the
first primer at its 3' end does not contain eleven or more bases that are perfectly matching
15 except one mismatch to a sequence anywhere of the first primer or the second primer.
2. A method of claim 1 wherein at least 100 primers are designed.
3. A method of claim 2 wherein at least 200 primers are designed.
4. A method of claim 3 wherein at least 1000 primers are designed.
5. A method of claim 1 wherein at least 50 target DNA fragments are produced
20 in the single multiplex polymerase chain reaction.
6. A method of claim 1 wherein at least 100 target DNA fragments are produced
in the single multiplex polymerase chain reaction.

7. A method of claim 1 wherein at least 500 target DNA fragments are produced in the single multiplex polymerase chain reaction.

8. A method of claim 1 wherein the single multiplex polymerase chain reaction is used for an application.

5 9. A method of claim 8 wherein the application is selected from the group consisting of an identification of multiple genes related to multifactorial diseases, a genome-scale detection of genetic alterations in cancers, a study in large-scale pharmacogenetic reactions, a genotyping genetic polymorphism in a large population, and a gene expression profiling.

10 10. A method of claim 1 wherein the primers increase the efficacy of the single multiplex polymerase chain reaction.

11. A method of claim 1 wherein the primers minimize the non-specific extension of the single multiplex polymerase chain reaction.

12. A computer product comprising a computer readable medium containing a
15 computer program which once executed by a computer processor performs the method of claims 1-11.

5' CGATCGTACGATCGATCGATC
3' AGCTAGGCTCTAGGCATTG

Perfect match of 3'-

5' CGATCGTACGATTCTGATCAGA
3' AGCTAGGCTCTAGGCATTG

Perfect match of 3'-ends except on

5' CGATCGTACAACGAGATCCG
3' AGCTAGGCTCTAGGCATTGCATTG

3'-end of one primer perfect matches
any sequence of the other

5' CGATCGTACAACCCGAGCTCCG
3' AGCGAGGCTCTAGGCATTG

3'-end of one primer perfect matches any sequence but one base of the

5' CGATCCGATCCGAGATCCGTAAT
3' AGCTAGGCTCTACGCATTGCGACAGC

Maximal match between two primer

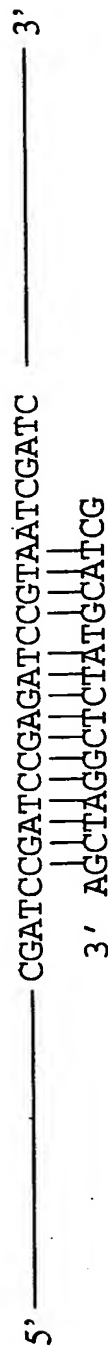
Fig. 1



3'-sequence of a primer perfectly matching a non-specific sequence amplified by other



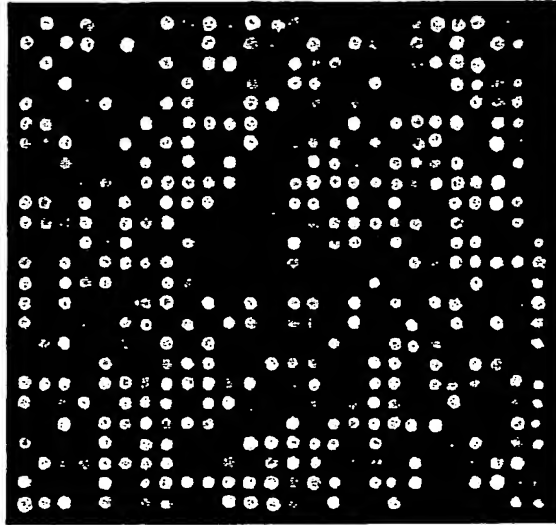
3'-sequence of a primer perfectly matching except one base with a non-specific sequence amplified by other primers



Maximal match between a primer sequence and a non-sequence amplified by other

Fig. 2

Red



Green

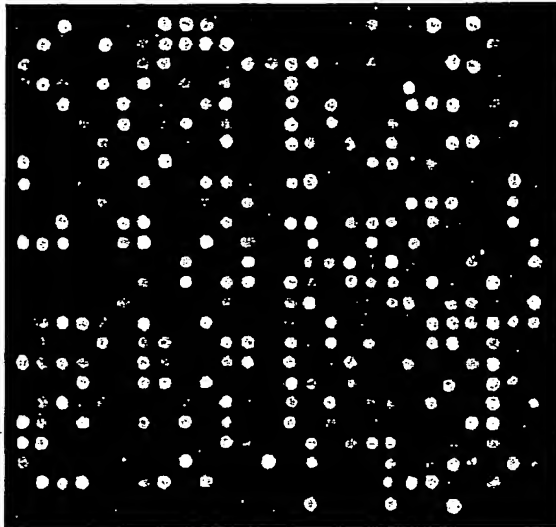


Fig. 3

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Criteria Used in Designing Primers That Are Experimentally Acceptable	
T _m Range of the primers (°C)	75-103
Length of the primers (bp)	24-33
Number of consecutive matching bases between the 3' ends of any two primer molecules	<4
Number of consecutive matching bases with one mismatch between the 3'-ends of any two primer molecules	<7
Number of consecutive matching bases between the 3'-end of one primer molecule and anywhere in another primer molecule	<9
Number of consecutive matching bases with one mismatch between the 3'-end of one primer molecule and anywhere in another primer molecule	<11
Maximal number of matching bases between two primer molecules	<75%
Number of consecutive matching bases between the 3'-end of a primer molecule and anywhere in a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	12
Number of consecutive matching bases with one mismatch between the 3'-end of a primer molecule and anywhere in a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	15
Maximal number of matching bases between a primer molecule and a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	<80%

Fig. 4